

crf 163903

Jarrell, Noble

From: Ramirez, Delia
Sent: Thursday, August 25, 2005 3:12 PM
To: Jarrell, Noble
Subject: FW: 09/598,982

-----Original Message-----

From: Ramirez, Delia
Sent: Monday, August 01, 2005 6:14 PM
To: Schreiber, David
Subject: 09/598,982

Hi,

I would like to request the following interference searches:

1. SEQ ID NO:52 in the protein and nucleic acid databases (commercial and interference)
2. SEQ ID NO:20 and 21 in the nucleic acid databases (interference)
3. SEQ ID NO:21 in the protein databases (interference)
4. an alignment of SEQ ID 9, 11, 21, 23, 25, 27, 37, 39, 41 and 43
5. an alignment of SEQ ID NO: 8, 10, 20, 22, 24, 26, 36, 38, 40, 42

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

Noble 8/31/05

Compuq 10/22

3/11/2006 10:00

Commercial
Interfer.

This Page Blank (uspto)

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 27, 2005, 21:12:24 ; Search time 607 Seconds

(without alignments)
2684.068 Million cell updates/sec

Title: US-09-598-982c-21

Perfect score: 1393
Sequence: 1 LERKIVGGQEPKRSKPMQV.....ITRTVYTYLDMHHYVKKP 249

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7311713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2_1/USPTO.spool/p/US095982c/Runat_25082005_165520_304/app.query.fasta_1.391
-DB=Published Applications NA -GFM=fastcap -SUFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIT=bits -SPART=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pcp -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcp -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US095982c@cgn2_1_723@runat_25082005_165520_304
-NCPU=6 -ICPU=3 -NO MMAP -LARGEOUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/2/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubna/US10D_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubna/US10E_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubna/US10F_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubna/US10G_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubna/US10H_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubna/US10I_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubna/US10J_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubna/US11_NEW_PUB.seq.*
23: /cgn2_6/ptodata/2/pubna/US11_PUBCOMB.seq.*
24: /cgn2_6/ptodata/2/pubna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	98.2	1143	17	US-10-352-684A-47 Sequence 47, Appl
2	1368	98.2	1145	18	US-10-287-226-93 Sequence 93, Appl
3	1368	98.2	1148	21	US-10-956-157-2444 Sequence 2444, Ap
4	1363	97.8	828	18	US-10-287-226-91 Sequence 91, Appl
5	1363	97.8	1193	21	US-10-956-157-1043 Sequence 1043, Ap
6	1355	97.3	1334	20	US-10-723-860-6799 Sequence 6799, Ap
7	1344	96.5	1081	9	US-09-954-456-1262 Sequence 2126, Ap
8	1344	96.5	1081	10	US-09-960-706-680 Sequence 680, App
9	1344	96.5	1081	10	US-09-873-319-427 Sequence 427, App
10	1344	96.5	1081	10	US-09-873-367C-155 Sequence 155, App
11	1344	96.5	1081	10	US-09-873-367C-714 Sequence 714, App
12	1344	96.5	1081	21	US-10-843-641A-155 Sequence 155, App
13	1344	96.5	1081	21	US-10-843-641A-714 Sequence 714, App
14	1344	96.5	1081	21	US-10-843-641A-5153 Sequence 5153, App
15	1329	95.4	2662	18	US-10-275-505-27 Sequence 27, Appl
16	1323	95.0	828	18	US-10-287-226-89 Sequence 89, Appl
17	1312	94.2	858	18	US-10-287-226-87 Sequence 87, Appl
18	1274	91.5	1154	17	US-10-352-684A-45 Sequence 45, Appl
19	1274	91.5	1158	14	US-10-116-802-240 Sequence 240, App
20	1274	91.5	1158	21	US-10-956-157-1042 Sequence 1042, Ap
21	1232	88.4	5456	20	US-10-723-860-2689 Sequence 2689, Ap
22	1232	88.4	5456	22	US-10-756-149-2484 Sequence 2484, Ap
23	1054	75.7	1187	18	US-10-275-505-22 Sequence 22, Appl
24	1005	72.1	729	21	US-10-480-988-55 Sequence 55, Appl
25	988	70.9	729	21	US-10-956-157-1789 Sequence 1789, Ap
26	958	68.8	600	21	US-10-956-157-7024 Sequence 7024, Ap
27	664.5	47.7	846	10	US-09-813-432-11 Sequence 11, Appl
28	664.5	47.7	846	17	US-10-174-364-11 Sequence 11, Appl
29	664.5	47.7	846	18	US-10-246-583-11 Sequence 11, Appl
30	664.5	47.7	846	19	US-10-689-832-11 Sequence 2, Appl
31	634	45.5	873	14	US-10-117-323-2 Sequence 1, Appl
32	605.5	43.5	1122	9	US-09-900-754-1 Sequence 15, Appl
33	599.5	43.0	948	16	US-10-131-409-15 Sequence 15, Appl
34	599.5	43.0	948	17	US-10-139-854-15 Sequence 15, Appl
35	599.5	43.0	948	17	US-10-150-813-15 Sequence 15, Appl
36	599.5	43.0	948	17	US-10-150-811-15 Sequence 15, Appl
37	593.5	42.6	1199	21	US-10-956-157-1816 Sequence 1816, Ap
38	584	41.9	978	15	US-10-311-955-1 Sequence 1, Appl
39	583.5	41.9	1958	17	US-10-311-935-29 Sequence 29, Appl
40	569.5	40.9	666	21	US-10-956-157-5078 Sequence 5078, Ap
41	569.5	40.9	867	9	US-09-888-615-56 Sequence 56, Appl
42	569.5	40.9	895	14	US-10-117-323-34 Sequence 34, Appl
43	569.5	40.9	1218	17	US-10-274-639-36 Sequence 36, Appl
44	569.5	40.9	1218	18	US-10-333-574-36 Sequence 36, Appl
45	568	40.8	858	16	US-10-131-409-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-352-684A-47
; Sequence 47, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 178822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019P1R0NMIM

```

CURRENT APPLICATION NUMBER: US/10/352,684A
CURRENT FILING DATE: 2003-01-28
PRIORITY APPLICATION NUMBER: US 60/354,333
PRIORITY FILING DATE: 2002-02-04
PRIORITY APPLICATION NUMBER: US 60/360,258
PRIORITY FILING DATE: 2002-02-28
PRIORITY APPLICATION NUMBER: US 60/364,476
PRIORITY FILING DATE: 2002-03-15
PRIORITY APPLICATION NUMBER: US 60/375,626
PRIORITY FILING DATE: 2002-04-26
PRIORITY APPLICATION NUMBER: US 60/386,494
PRIORITY FILING DATE: 2002-06-06
PRIORITY APPLICATION NUMBER: US 60/390,965
PRIORITY FILING DATE: 2002-06-24
PRIORITY APPLICATION NUMBER: US 60/392,480
PRIORITY FILING DATE: 2002-06-28
PRIORITY APPLICATION NUMBER: US 60/394,128
PRIORITY FILING DATE: 2002-07-03
PRIORITY APPLICATION NUMBER: US 60/399,783
PRIORITY FILING DATE: 2002-07-31
PRIORITY APPLICATION NUMBER: US 60/403,221
PRIORITY FILING DATE: 2002-08-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO 47
LENGTH: 1143
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(833)
US-10-352-684A-67

```

Alignment Scores:	
Pred. No.:	2,05e-158
Score:	1368.00
Percent Similarity:	99.59%
Best Local Similarity:	99.59%
Query Match:	96.21%
DB:	17
US-09-598-982C-21 (1-249) x US-10-352-684A-47 (1-1143)	
	length: 1143
	Matches: 244
	Conservative: 0
	Mismatches: 1
	Indels: 0
	Gaps: 0

QY	5	lleValGlgYlGlgInlunlaProkarselvtstPpPpGlnValserLeuVal	24
Db	96	ATGTTGGGGGTCAGAGGCCCCCAGAGCAAGTGGCTTGCGAGTGAAGCTCAAGTGC	155
QY	25	HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu	44
Db	156	CAGGGCCCATCTGATGATGATCTTCTCGGGGGGCTCCCTCATCCACCCCAAGTGGTCTG	215
QY	45	ThrAlaAlaAlaCysValGlyProAspValIlyAspLeuAlaAlaLeuArgValGlnLeu	64
Db	216	ACCGCAGCCACCTGCGTGGAGCCGAGACGTCAAGATCTGGCGGCTCCAGGGTCAACTG	275
QY	65	ArgGlnGlnHisIleuLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleIleValHis	84
Db	276	CGGAGCAGACACTCTACTACAGAGCAACGCTGCTCGCGGTACAGAGGATATGTGCAC	335
QY	85	ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro	104
Db	336	CCACAGTTTCAACCGCCGACATCGGAGGGACATCGCCCTGTGGAGCTGAGAGACCG	395
QY	105	ValIysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro	124
Db	396	GTAAGAGTTCAGAGCAGCTCCACAGGTCACCTCGCCCCCTGCTCAGAAACCTTCCC	455
QY	125	ProGlnMetProCysTrpValThrGlyTrpGlyAspValAlaAspAspGluArgLeuPro	144
Db	456	CCGGGATGCGCTGCTGGGATCACTGGCTGGGGCATGTGGACAATGATGAGCGCTCCA	515
QY	145	ProProPheProLeuLysGlnValIlyValProIleMetGluAsnHisIleCysAspAla	164

Db	516	CCGCCATTTCTCTAGACAGGTGAAGTCCCCATTAATGGAAAAACCACTTTTGAAGCA	575
QY	165	LYSTYTHILEUGLYALATYTHTCIYASAPAYALArgIleValAlaGAPAPMetLeu	184
Db	576	AAATACACCTTGCGCCTTACACGGGAGACAGCTCGGCATCGTCCGTGACGACATGCTG	635
QY	185	CYVALAGLYASHTHAYGARGAPSerCy66InIlyAPSerGIyGIYProIleuValCY6	204
Db	636	TGGCCGGGAAACCCGGAGGAGTCAATGCCAGGCGCATTCGGAGGGCCCCGTGGTGTGC	695
QY	205	LYSVALASNGIYTHTRPLeuGlnAlaGlyValAlaIleTTPGlyGlnGIYCYVALAGIn	224
Db	696	AAGTGAATGGCACTGGCTGCAGGGCGGCGTGGTCAAGCTGGGGCAGAGGCTGTGCCAG	755
QY	225	PROASHPAPGCGIYIleTYTHrArgValIThrTYTLeuAPTrpIleHisIstYr	244
Db	756	CCCAACCGGCGCTGGCATCTAACCCGGTGTCACTACTGACTGGACTGGATCCACCACTAT	815
QY	245	VALProLYLeuPPro	249
Db	816	GTTCCTCCAAAAAGCCG	830

RESULT 2
 US-10-287-226-93
 Sequence 93. Application US/10287226
 Publication No. US20040086875A1
 GENERAL INFORMATION:
 APPLICANT: Agee, Michele L.,
 APPLICANT: Alsobrook, John P.,
 APPLICANT: Berghs, Constance,
 APPLICANT: Boldog, Ferenc,
 APPLICANT: Burgess, Catherine E.,
 APPLICANT: Chant, John S.,
 APPLICANT: Chaudhuri, Amitabha,
 APPLICANT: DiPippo, Vincent A.,
 APPLICANT: Edinger, Shlomit R.,
 APPLICANT: Eissen, Andrew,
 APPLICANT: Ellerman, Karen,
 APPLICANT: Gangolli, Esna A.,
 APPLICANT: Gorman, Linda,
 APPLICANT: Gerlach, Valerie,
 APPLICANT: Ji, Weizhen,
 APPLICANT: Kekuda, Ramesh,
 APPLICANT: Khramtsov, Nikolai,
 APPLICANT: Li, Li,
 APPLICANT: Malyankar, Uriel M.,
 APPLICANT: MacDougall, John R.,
 APPLICANT: Mezes, Peter S.,
 APPLICANT: Miller, Charles E.,
 APPLICANT: Millet, Isabelle,
 APPLICANT: Ooi, Chean Eng,
 APPLICANT: Ort, Tatiana,
 APPLICANT: Padigaru, Muralidhara,
 APPLICANT: Patuturajan, Meera,
 APPLICANT: Rascelli, Luca,
 APPLICANT: Rieger, Daniel K.,
 APPLICANT: Rothenberg, Mark E.,
 APPLICANT: Shenoy, Suresh G.,
 APPLICANT: Spaderna, Steven K.,
 APPLICANT: Spytek, Kimberley A.,
 APPLICANT: Taupier, Jr., Raymond J.,
 APPLICANT: Vernet, Corine A.M.,
 APPLICANT: Zernusen, Bryan D.,
 APPLICANT: Zhong, Mei
 TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 21402-480C
 CURRENT APPLICATION NUMBER: US/10/287,226
 CURRENT FILING DATE: 2002-11-04
 PRIOR APPLICATION NUMBER: 60/334,421
 PRIOR FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: 60/354,392
 PRIOR FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: 60/360,148
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/404,821
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 60/334,526
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/354,409
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/364,227
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/331,641
PRIOR FILING DATE: 2001-11-20
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 673
SOFTWARE: CuroSeqList version 0.1
SEQ ID NO 93
LENGTH: 1145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (8)..(832)
US-10-287-226-93

Alignment Scores:

Pred. No.:	2,06e-158	Length:	1145
Score:	1368.00	Matches:	244
Percent Similarity:	99.59%	Conservative:	0
Best Local Similarity:	99.59%	Mismatches:	1
Query Match:	98.21%	Indels:	0
DB:	18	Gaps:	0

US-09-598-982c-21 (1-249) x US-10-287-226-93 (1-1145)

QY 5 ILevalGlyGlnGluAlaProArgSerLyTrpProTrpGlnValSerLeuArgVal 24
DB 98 ATCGTTGGGGGTCAAGAGGCCCCAGAGCAAGTGGCCCTGAGGTGAGAGTGC 157
QY 25 HIsGlyProTyTrpMetHisPheCysGlyGlySerLeuLeuHisProGlnTrpValLeu 44
DB 158 CACGGCCCATCTGATGACTTCTGCGGGGCTCCCTATCACCCCACTGGGTGCTG 217
QY 45 ThrAlaAlaCysValGlyProArgValLysAspLeuAlaAlaLeuArgValGlnLeu 64
DB 218 ACCGAGGCCACTGCTGTGGACCGGACGTCAGAGATCTGGCCCTCAGGATGCACTG 277
QY 65 ArgGlnGlnHisLeuTyTrpGlnAspGlnLeuProValSerArgIleIleValHis 84
DB 278 CGGAGGACGACCTCTACTACAGGACAGCTGCTGCCGTGACAGATCATGTCGAC 337
QY 85 ProGlnPheTyTrpAlaGlnIleGlyAlaAspIleAlaLeuGlnLeuGlnGluPro 104
DB 338 CCACAGTTTACACGCGCCAGATCGAGGCAATGCTCTGTGAGTGAAGAGCGG 397
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
DB 398 GTGAAGGTTCACAGCAGCTCCACAGCTCACCTGCCCCCTCAGAGATCTTCCCC 457
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspAspGluArgLeuPro 144
DB 458 CCGGGGATCCCGTGGCTGCTACTGCTGGGGGAGTGGAGCAATGATAGGCGCTCCA 517
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAspHisIleCysAspAla 164
DB 518 CCGCAATTCCTCTGAAGAGGTGAAGTCCCATATATGAAGAACCACTTTGTAGCGCA 577
QY 165 LySTyHisLeuGlyValAlaTyTrpGlyAspAspValArgIleValArgAspAspMetLeu 184
DB 578 AATATACCACTTGGGGCGCTACACGGGAGAGAGATGCTCGCATCTCGTACAGCATGCTG 637

QY 185 CysAlaGlyAsnThrArgArgSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
DB 638 TGTCCGGGAACACCCGAGGAGCTCATGCCAGGCACTCCGAGGGCCCTGTGTGTC 697
QY 205 LySValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlnGlyCysAlaGln 224
DB 698 AAGGTGAATGCACTGCTGTCACAGCGGGGTGTGAGCTGGGGCGAGGGCTGTGCCAG 757
QY 225 ProAsnArgProGlyIleTyTrpThrArgValThrTyTrpLeuAspTrpIleHisIleTy 244
DB 758 CCAACCGGCTGCGATCTACACCCGCTGCTACTACTTGAATGCACTGATCCACACTAT 817
QY 245 ValProLysLysPro 249
DB 818 GTCCCAAAAAGCCG 832

RESULT 3

US-10-956-157-2444
Sequence 2444, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2444
LENGTH: 1148
TYPE: DNA
ORGANISM: Homo sapiens
US-10-956-157-2444

Alignment Scores:

Pred. No.:	2,06e-158	Length:	1148
Score:	1368.00	Matches:	244
Percent Similarity:	99.59%	Conservative:	0
Best Local Similarity:	99.59%	Mismatches:	1
Query Match:	98.21%	Indels:	0
DB:	21	Gaps:	0

US-09-598-982c-21 (1-249) x US-10-956-157-2444 (1-1148)

QY 5 ILevalGlyGlnGlnAlaProArgSerLyTrpProTrpGlnValSerLeuArgVal 24
DB 98 ATCGTTGGGGGTCAAGAGGCCCCAGAGCAAGTGGCCCTGAGGTGAGAGTGC 157
QY 25 HIsGlyProTyTrpMetHisPheCysGlyGlySerLeuLeuHisProGlnTrpValLeu 44
DB 158 CACGGCCCATCTGATGACTTCTGCGGGGCTCCCTATCACCCCACTGGGTGCTG 217
QY 45 ThrAlaAlaCysValGlyProArgValLysAspLeuAlaAlaLeuArgValGlnLeu 64
DB 218 ACCGAGGCCACTGCTGTGGACCGGACGTCAGAGATCTGGCCCTCAGGATGCACTG 277
QY 65 ArgGlnGlnHisLeuTyTrpGlnAspGlnLeuProValSerArgIleIleValHis 84
DB 278 CGGAGGACGACCTCTACTACAGGACAGCTGCTGCCGTGACAGATCATGTCGAC 337
QY 85 ProGlnPheTyTrpAlaGlnIleGlyAlaAspIleAlaLeuGlnLeuGlnGluPro 104
DB 338 CCACAGTTTACACGCGCCAGATCGAGGCAATGCTCTGTGAGTGAAGAGCGG 397
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
DB 398 GTGAAGGTTCACAGCAGCTCCACAGCTCACCTTGGCCCCCTGCTCAGAGATCTTCCCC 457
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspAspGluArgLeuPro 144

Db	458	CCGGGAGATGCCGCGTGGGTCACTGGCTGGGGCATGTGGACAATGATGAGAGCGCTCCA	51
Qy	145	ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla	166
Db	518	CCCCCATTTCTCTGTGAAGCAGGGAAAGGTCGCCCATATGGAAGAAACCATTTGTGGAGCA	577
Qy	165	LysTyrHisIleuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys	186
Db	578	AAATATCCACTTGGCGCTTACACGGGAGACGACGTCCGATGTCTCCGAGACCATCTGG	637
Qy	185	CysAlaGlyAsnThrArgArgAspSerCysGlnGlyLysAspSerGlyProLeuValCys	204
Db	638	TGTGCCGGGAACACCCGGAGGACTATATCCACAGGCGACTCCGAGAGGCCCTCTGTGTGC	697
Qy	205	LysValAsnGlyThrTrpLeuGlnAlaGlyValLysSerTrpGlyGlnGlyCysAlaGln	224
Db	698	AAGGTGATGGCACCCTGGCTGCAGCGGGCGTGTGACGTGGGGGAGAGGGCTGTGGCCAG	757
Qy	225	ProAsnArgProGlyLysIleTyrThrArgValThrTyrTrpLeuAspTrpIleHisHisTyr	244
Db	758	CCCAACCGGCGCTGGCATCTACACCCCTGTCACTTACTTGGAGTCGATCCACCACTAT	817
Qy	245	ValProLysLysPro	249
Db	818	GTCCCCAAAAAGCCG	832

RESULT 4

US-10-287-226-91
; Sequence 91, Application US/10287226
; Publication No. US20040086875A1

GENERAL INFORMATION:

APPLICANT: Agee, Michele L.,
 APPLICANT: Alsobrook, John P.,
 APPLICANT: Berghs, Constance,
 APPLICANT: Boldog, Ference,
 APPLICANT: Burgess, Catherine E.,
 APPLICANT: Chan, John S.,
 APPLICANT: Chaudhuri, Amitabha,
 APPLICANT: DiPippo, Vincent A.,
 APPLICANT: Edinger, Shlomit R.,
 APPLICANT: Eisen, Andrew,
 APPLICANT: Eilerman, Karen,
 APPLICANT: Gangolli, Bsha A.,
 APPLICANT: Gorman, Linda,
 APPLICANT: Gerlach, Valerie,
 APPLICANT: Ji, Weizhen,
 APPLICANT: Kekkda, Ramesh,
 APPLICANT: Khrantsov, Nikolai,
 APPLICANT: Li, Li,
 APPLICANT: Malyankar, Uriel M.,
 APPLICANT: Macdougall, John R.,
 APPLICANT: Mezes, Peter S.,
 APPLICANT: Miller, Charles E.,
 APPLICANT: Miller, Isabelle,
 APPLICANT: Ooi, Chean Eng,
 APPLICANT: Ort, Tatiana,
 APPLICANT: Padigaru, Muralidhara,
 APPLICANT: Patturajan, Meera,
 APPLICANT: Rastelli, Luca,
 APPLICANT: Rieger, Daniel K.,
 APPLICANT: Rothenberg, Mark E.,
 APPLICANT: Shenoy, Suresh G.,
 APPLICANT: Spaderna, Steven K.,
 APPLICANT: Szytek, Kimberley A.,
 APPLICANT: Taupier, Jr., Raymond J.,
 APPLICANT: Varner, Corine A.M.,
 APPLICANT: Zerhusen, Bryan D.,
 APPLICANT: Zhong, Mei
 TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 21402-460C
 CURRENT APPLICATION NUMBER: US/10/287,226
 CURRENT FILING DATE: 2002-11-04
 PRIOR APPLICATION NUMBER: 60/334,421

```

? PRIOR FILING DATE: 2001-11-30
? PRIOR APPLICATION NUMBER: 60/354,392
? PRIOR FILING DATE: 2002-02-04
? PRIOR APPLICATION NUMBER: 60/360,148
? PRIOR FILING DATE: 2002-02-27
? PRIOR APPLICATION NUMBER: 60/364,000
? PRIOR FILING DATE: 2002-03-13
? PRIOR APPLICATION NUMBER: 60/404,821
? PRIOR FILING DATE: 2002-08-20
? PRIOR APPLICATION NUMBER: 60/334,526
? PRIOR FILING DATE: 2001-11-30
? PRIOR APPLICATION NUMBER: 60/354,409
? PRIOR FILING DATE: 2002-02-04
? PRIOR APPLICATION NUMBER: 60/364,227
? PRIOR FILING DATE: 2002-03-13
? PRIOR APPLICATION NUMBER: 60/334,027
? PRIOR FILING DATE: 2001-11-28
? PRIOR APPLICATION NUMBER: 60/331,641
? PRIOR FILING DATE: 2001-11-20
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 673
? SOFTWARE: Curaseqdist version 0.1
? SEQ ID NO 91
?
? LENGTH: 828
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? FEATURE:
?
? NAME/KEY: CDS
?
? LOCATION: (1)..(825)
US-10-287-226-91

```

Alignment Scores:

Pred. No.:	5,54e-158	Length:	828
Score:	1363.00	Matches:	213
Percent Similarity:	99.18%	Conservative:	0
Best Local Similarity:	99.18%	Mismatches:	2
Query Match:	97.85%	Indels:	0
DB:	18	Gaps:	0
US-09-5598-982C-21 (1-249) x US-10-287-226-91 (1-628)			

Oy	5	ILEVALGIYGIYGLINGIUALAProAGserLTySTPProTgPInValSerLeuArgVal	24
Db	91	ATGCTGGGGGGGTGAGAGAGCCCCCAGAGCAAGTGGCCCTGGCAGGTAGCTGAGACT	15
Oy	25	HISGLYProTYrTPwethiSpheCySGIYGLYSerLeuIleHisProGLnTPyValLeu	44
Db	151	CAGGGCCCAATCGATGACCTTCTGGGGGGCTCCCTCATCCACCCCAAGGGGTGGCTG	21
Oy	45	ThnAlaIaIaIaCySValGIYProAspValIlyAspLeuAlaIleuArgValGlnLeu	64
Db	211	ACCGCAGCGACACTGGCTGGGACCGGACGCTCAAGACTTGGCCGCCCTCAGGGTGCMACTG	27
Oy	65	ArgGLnGlnHisLeuTYrTYrGlnAspGlnLeuLeuProValSerArgIleIleValHis	84
Db	271	CGGAGCAGACACTTACTACAGGACCGACTGGCTGGCGGTACGACGAGATATCTGTGAC	33
Oy	85	ProGLnPhenTYrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlnLeuGlnPro	10
Db	331	CCACAGTTCTTACACCGCCAGATCGAGCGGAGACATCGCCCTCTGTAAGCTGAGAGCCG	39
Oy	105	ValIyValSerSerHisValHisThrValIThrLeuProProIaISerGIuThrPhePro	12
Db	391	GTGAAGCTCTCCAGCACAAGCCACAAGGTCACCTTGCCCCCTCGCTCAGAGACCTTCCCC	45
Oy	125	ProGLwHerProCySTyTPyValIThrGIYTPGIIyAspValAspAsnArgGluArgLeuPro	14
Db	451	CCGGGAGTGGCGTGGTGGCTCACTGGCTGGGGGAGATGTGACATGATGAGGCTCCCA	51
Oy	145	ProProHebProLeuIySGInValIlyValProIleMeGLuAsnHisIleCySAspAla	16
Db	511	CCGCACATTTCTCTGTGAAGCAGGTGAAGTCCCCCATATGTGAAGAAACCAATTTGTGACCA	57

```
QY 165 LysTyrHisLeuGlyValaThrGlyAspAspValArgIleValArgAspAspMetLeu 184
DB 571 AAATACCACTTGCGGCTACAGGAGAGAGCGATCGCATGCTCGTGAACAATGCTG 630
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
DB 631 TGTGCGGGGAACACCCGGAGGAGATCTCATCCAGGGGAGATCCGGAGGGGCGCTGGTGTGC 690
QY 205 LysValaAenGlyThrTrpLeuGlnaGlyValaValaSerTrpGlyGlnGlyCysAlaGln 224
DB 691 AAGGTGAATGGACCTGGCTGAGGCGGCGGTGTCAGCTGGGCGAGGGCTGTGCTCCAG 750
QY 225 ProAsnArgProGlyIleTyrThrArgValaThrTyrTyrLeuAspTrpIleHisIstYr 244
DB 751 CCAACCGGCTGGCATCTACACCGGTGTCACCTACTGACTGATGATCCACCATAT 810
QY 245 ValProLysLysPro 249
DB 811 GTCCCAAAAAGCCG 825

RESULT 5
US-10-956-157-1043
; Sequence 1043, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mount, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1043
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-1043

Alignment Scores:
Pred. No.: 9e-158 Length: 1193
Score: 1363.00 Matches: 243
Percent Similarity: 99.18% Conservative: 0
Best Local Similarity: 99.18% Mismatches: 2
Query Match: 97.85% Indels: 0
Gaps: 0
DB: 21

US-09-598-982c-21 (1-249) x US-10-956-157-1043 (1-1193)
QY 5 11eValGlyGlnGlnAlaProArgSerLySTrProTrpGlnValSerLeuArgVal 24
DB 143 ATGTCGCGGGGTACAGAGGCGCCCGAGAGCAAGTGCGCTGAGGTGAGTCAAGTGC 202
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
DB 203 CACGGGCGCACTGAGTGAATGACTTCTGCGGGGCGCTCCCTATCAACCCCAAGTGGGCTG 262
QY 45 ThrAlaAlaAlaCysValaGlyProAspValLysAspLeuAlaAlaLeuArgValaGlnLeu 64
DB 263 ACCGAGCGCCACTGCTGGAGACCGAGCTCAAGAGATCTGGCGGCTCGAGGTGCACTG 322
QY 65 ArgGlyGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
DB 323 CCGGAGCAACACTCTACTACTACAGAGACAGCTGCTGCTGCTGAGCAGATCTGCTGAC 382
QY 85 ProGlnPheTyrThrIleGlnIleGlyAlaAspIleAlaLeuLeuGlnLeuGlnGlyPro 104
DB 383 CCACTCTTCAACCGCCCAAGTGGAGGAGATCGCTGCTGAGTGGAGGAGCGG 442
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGlyThrPhePro 124
DB 443 GTGAAGCTCTCCAGCGCATCCACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 502
```

```
QY 125 ProGlyMetProCysTrpValaThrGlyTrpGlyAspValaAspAspGlnaArgLeuPro 144
DB 503 CCGGGAGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
QY 145 ProProPheProLeuLysGlnValaLysValaProIleMetGluAsnHisIleCysAspAla 164
DB 563 CCGCATTTCTCTGGAAGCAGTGAAGTCCCATTAATGAAACCAACATTTGTGAGCGCA 622
QY 165 LysTyrHisLeuGlyValaTyrThrGlyAspAspValaArgIleValaArgAspAspMetLeu 184
DB 623 AAATACCACTTGCGGCTTACACCGGAGACACACCTCCGATGTCCTGGAGACATGCTG 682
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
DB 683 TGTGCGGGGAACACCCGGAGGAGATCTCATCCAGGAGCGACTCCGAGGGGCGCTGGTGTGC 742
QY 205 LysValaAenGlyThrTrpLeuGlnaGlyValaValaSerTrpGlyGlnGlyCysAlaGln 224
DB 743 AAGGTGAATGGACCTGGCTGAGGCGGCGGTGTCAGCTGGGCGAGGGCTGTGCTCCAG 802
QY 225 ProAsnArgProGlyIleTyrThrArgValaThrTyrTyrLeuAspTrpIleHisIstYr 244
DB 803 CCAACCGGCTGGCATCTACACCGGTGTCACCTACTGACTGATGATCCACCATAT 862
QY 245 ValProLysLysPro 249
DB 863 GTCCCAAAAAGCCG 877

RESULT 6
US-10-723-860-6799
; Sequence 6799, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6799
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-6799

Alignment Scores:
Pred. No.: 1.02e-156 Length: 1334
Score: 1355.00 Matches: 242
Percent Similarity: 98.78% Conservative: 0
Best Local Similarity: 98.78% Mismatches: 3
Query Match: 97.27% Indels: 0
Gaps: 0
DB: 20

US-09-598-982c-21 (1-249) x US-10-723-860-6799 (1-1334)
QY 5 11eValGlyGlnGlnAlaProArgSerLySTrProTrpGlnValSerLeuArgVal 24
DB 143 ATGTCGCGGGGTACAGAGGCGCCCGAGAGCAAGTGCGCTGAGGTGAGTCAAGTGC 202
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
DB 203 CCGGCGCACTGAGTGAATGACTTCTGCGGGGCGCTCCCTATCAACCCCAAGTGGGCTG 262
QY 45 ThrAlaAlaAlaCysValaGlyProAspValLysAspLeuAlaAlaLeuArgValaGlnLeu 64
DB 263 ACCGAGCGCACTGCTGGAGACCGGAGCTCAAGAGATCTGGCGGCTCGAGGTGCAACTG 322
```



```

; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 680
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 M33493
US-09-960-706-680

Alignment Scores:
Pred. No.: 1,75e-155 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: 10 Gaps: 0

US-09-598-982c-21 (1-249) x US-09-960-706-680 (1-1081)
QY 5 ILevalGIyGIyGlnGlnAlaProAArgSerIySTPProTglnValSerIeuArgVal 24
Db ATCGTTGGGGGTCAGAGAGCCCCCAGAGCAAGTGCCTCGAGGTGAGCTGAGAGTC 127
QY 25 HisGIyProTyTTrpMetHisPheCySGIyGIySerIeuIleHisProGlnTrpValIeu 44
Db CGCGACCGATCTGATGATGACATCTCGGGGGCTCCCTATCATCCCCAGTGGGTGCTG 187
QY 45 ThrAlaAlaAlaCyValGlyProAArgValIyAspIeuAlaIleuArgValGlnIeu 64
Db ACCGAGCGCAGCTGCGTGGGACCGGACGTCAAGATCTGCGCCCTCAGGGTGAACATG 247
QY 188 ACCGAGCGCAGCTGCGTGGGACCGGACGTCAAGATCTGCGCCCTCAGGGTGAACATG 247
QY 65 ArgGIuGlnHisIeuTyTTrpGlnAspIeuProValSerArgIleIleValHis 84
Db CGGAGGACGACCTCTACTACAGAGCCAGCTGCGTCCGCTGAGAGGATCATCGGCAC 307
QY 85 ProGlnPheTyTTrpAlaGlnIleGlyAlaAspIleAlaIleuIeuGlnIeuPro 104
Db CCACAGTTCTTACACCGCCAGATCGAGCGGACATCGCTCTGAGAGCTGAGAGCGC 367
QY 105 ValIyValSerSerHisValHisThrValIThrIeuProAlaSerGIuThrPhePro 124
Db GTGAAGGTCTCCAGCCAGCTCCACACGTCACCTGCCCCCTCAGAGACTTTCCCC 427
QY 125 ProGIyMetProCySTrPValIThrGIyTTrpGIyAspValIAspAsnAspGIuArgIeuPro 144
Db CCGGGGATCCCGTGTGGGTCACTGCTGGGCGAGATGAGCAATGATAGAGGCCCTCCCA 487
QY 145 ProProPheProIeuIyGlnValIyValProIleMetGIuAsnHisIleCyAspAla 164
Db CCGCCATTTCTCTGAGAGAGGTGAGAGTCCCATATATGAAACCACTTTGTGAGCA 547
QY 165 IySTyHisIeuGIyAlaTyTThrGIyAspAspValArgIleValArgAspAspIeu 184
Db AATATACACTTGTGGGCTTACAGGAGAGGAGAGTCCGATCGCTGAGAGCAATGCTG 607
QY 185 CyAlaGIyAsnThrArgArgAspSerCyGlnGIyAspSerGIyGIyProIeuValCys 204
Db TGTGCGGAGAACCCCGAGGAGCTCATGCTCAGGGGAGCATCCGAGAGGCCCTGTGTC 667
QY 205 IyValIAsnGIyTThrIleuGlnIleGlyValIValSerTTrpGIyGIyGIyCysAlaGln 224

```

```

Db 668 AAGGTGATGGCACCTGAGCGAGCGCGGTGAGCTGGGGGAGAGGCTGTGCCAG 727
QY 225 ProAenArgProGIyIleTyTThrArgValIThrTyTyrIeuAspTrpIleHisTyTyr 244
Db CCACACGGGCTGTGACATCTACACCGGTGATCCTACTTGTGAGCTGATCCACACTAT 787
QY 245 ValProIySIyAspPro 249
Db GTCCCAAAAAAGCCG 802

RESULT 9
US-09-873-319-427
; Sequence 427, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; PRIOR FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 427
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 M33493
US-09-873-319-427

Alignment Scores:
Pred. No.: 1,75e-155 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: 10 Gaps: 0

US-09-598-982c-21 (1-249) x US-09-873-319-427 (1-1081)
QY 5 ILevalGIyGIyGlnGlnAlaProAArgSerIySTPProTglnValSerIeuArgVal 24
Db ATCGTTGGGGGTCAGAGAGCCCCCAGAGCAAGTGCCTCGAGGTGAGCTGAGAGTC 127
QY 25 HisGIyProTyTTrpMetHisPheCySGIyGIySerIeuIleHisProGlnTrpValIeu 44
Db CGCGACCGATCTGATGATGACATCTCGGGGGCTCCCTATCATCCCCAGTGGGTGCTG 187
QY 45 ThrAlaAlaAlaCyValGlyProAArgValIyAspIeuAlaIleuArgValGlnIeu 64
Db ACCGAGCGCAGCTGCGTGGGACCGGACGTCAAGATCTGCGCCCTCAGGGTGAACATG 247
QY 188 ACCGAGCGCAGCTGCGTGGGACCGGACGTCAAGATCTGCGCCCTCAGGGTGAACATG 247
QY 65 ArgGIuGlnHisIeuTyTTrpGlnAspIeuProValSerArgIleIleValHis 84
Db CGGAGGACGACCTCTACTACAGAGCCAGCTGCGTCCGCTGAGAGGATCATCGGCAC 307
QY 85 ProGlnPheTyTTrpAlaGlnIleGlyAlaAspIleAlaIleuIeuGlnIeuPro 104
Db CCACAGTTCTTACACCGCCAGATCGAGCGGACATCGCTCTGAGAGCTGAGAGCGC 367
QY 105 ValIyValSerSerHisValHisThrValIThrIeuProAlaSerGIuThrPhePro 124
Db GTGAAGGTCTCCAGCCAGCTCCACACGTCACCTGCCCCCTCAGAGACTTTCCCC 427
QY 125 ProGIyMetProCySTrPValIThrGIyTTrpGIyAspValIAspAsnAspGIuArgIeuPro 144

```


Db 428 CCGGGATGCGCTGCTGGGTCACTGGCTGGGGCGATGTGACATGATGACGCGCTCCCA 487
Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 488 CCGCCATTTCCTCTGAAGACAGGTGAAGGTCCCATATGGAACAAACACTTTGTGACGA 547
Qy 165 LysTyrHisLeuGlnValaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
Db 548 AATATACACCTTGCGCCCTACACGGAGACAGAGTCCGCATCTCCGTGACGACATGCTG 607
Qy 185 CysAlaGlyAsnThrArgAspAspSerCysGlnGlyAspSerGlyValLysProLeuValCys 204
Db 608 TGTCGGGGGAACCCGGAGGGACTGATGCGAGGCGACTCCGGAGGGCCCCCTGGTGTGC 667
Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db 668 AAGGTAAATGGCACCTGGCTGGAGGGGGGTGTGTGACGTGGGGCGAAGGGCTGTGCCAG 727
Qy 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
Db 728 CCCAACCGGCTGTGGCATCTACACCGGTGTCACTTGTGAGCTGATCCACCATAT 787
Qy 245 ValProLysLysPro 249
Db 788 GTCCCAAAAAGCCG 802

RESULT 10

US-09-873-367C-155
; Sequence 155, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 155
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-155

Alignment Scores:

Pred. No.: 1,75e-155 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: 10 Gaps: 0

US-09-598-982C-21 (1-249) x US-09-873-367C-155 (1-1081)

Qy 5 lIeValGlyGlnGlnLunAProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db 68 ATGCTGGGGGGGTGAGAGGCCCCACAGACCAAGTGGCTCGGAGGTGAGCTGAGAGTGC 127
Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44

Db 128 CCGGACCATCTGATGCATCTTCTGCGGGGGCTCCCTCATCCACCCCAAGGGTGTCTG 187
Qy 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
Db 188 ACCGAGCGCATCTGCTGGGACCGGACGTCAAGATCTGGCCGCTCAGGGTGCACCTG 247
Qy 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
Db 248 CCGGAGCAGACCTCTACTACCAAGACCAAGTGTGCGCGGTGACAGAGATCATCTGTGAC 307
Qy 85 ProGlnPheTyrThrAlaGlnIleGlyValAspIleAlaLeuGlnGlnLeuGlnLeu 104
Db 308 CCACAGTCTTACACCGCCGACATCGAGCGGACATCGGCTGTGACTGAGAGAGCGC 367
Qy 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGlyThrPhePro 124
Db 368 GTGAAGTCTCCAGCCACAGTCCACACGGTCACTGCGCCCTGTGCTCAGAGACTTCCCC 427
Qy 125 ProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAspGluArgLeuPro 144
Db 428 CCGGGGATGCGGTGTGGGTGACTGTGGGGCGATGTGACAAATGATGAGGCGCTCCCA 487
Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 488 CCGCCATTTCCTCTGAACAGGTGAAGTCCCATATGGAACAAACACTTTGTGACGCA 547
Qy 165 LysTyrHisLeuGlnValaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
Db 548 AATATCACCTTTGGGCGCTTACACGGAGACAGAGTCCCATGCTTCGAGACACATGCTG 607
Qy 185 CysAlaGlyAsnThrArgAspAspSerCysGlnGlyAspSerGlyValLysProLeuValCys 204
Db 608 TGTCGGGGGAACCCGGAGGGACTGATGCGAGGCGACTCCGGAGGGCCCCCTGGTGTGC 667
Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db 668 AAGGTAAATGGCACCTGGCTGGAGGGGGGTGTGTGACGTGGGGGAGGGCTGTGCCAG 727
Qy 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
Db 728 CCCAACCGGCTGTGGCATCTACACCGGTGTCACTTGTGAGCTGATCCACCATAT 787
Qy 245 ValProLysLysPro 249
Db 788 GTCCCAAAAAGCCG 802

RESULT 11

US-09-873-367C-714
; Sequence 714, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0


```

: SEQ ID NO 714
: LENGTH: 1081
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-873-367C-714

Alignment Scores:
Pred. No.: 1,75e-155 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservation: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: 10 Gaps: 0

US-09-598-982C-21 (1-249) x US-09-873-367C-714 (1-1081)

QY 5 ILEVALIGYGLVGLNGLUALAPROAAGSERLYETRPPTGPIVNAISERLEUARGVAL 24
DB 68 ATGCTTGGGGGTCAGAGAGCCCCCAGAGACAGATGAGCCCTTGACAGGTGAGCCTGAGATC 127
QY 25 HIAGLYPROTYRTPMETHIASPHECYSGLYGYSERLEULEHISPROGINTRPVALLEU 44
DB 128 CGGACCGCATCTGATGATGATCACTTCGCGGGGGCTCCCTCATCCACCCCAAGTGGTCTG 187
QY 45 THHALALALACYSVALIGLYPROASPVALYLSAPLEULALALEUARGVALINLEU 64
DB 188 ACCGACGACCATCTGCTGGAGACCGGACGTCAGATTCGGCGCCCTCAAGGTGCACTG 247
QY 65 ARGGLGLNHIISLEUETRYTGINAPGINLEUPEUPROVALSERARGILELEVALIHIS 84
DB 248 CGGAGACGACCTCTTACTACAGACAGACAGCTGCTCGGATCAGAGATCATGTGTCAC 307
QY 85 PROGLNPHETRYTHRALAGNILEGLVALASPILEALEULEUGIULEUGIUPRO 104
DB 308 CCACAGTTCTACACCGCCCAAGTCCGAGAGGACATCGCCCTGCTGAGAGCTGAGAGACCG 367
QY 105 VALLYEVALISERSEHISVALHISTHRVALTHRIEUPROPFOALASERGIUTHPHETRO 124
DB 368 GTGAAAGTCTCCAGCCACCTCCACAGCTGACCTCGCCCTGCTCAGAGACCTTCC 427
QY 125 PROGLYMETPROCYETTRPVALTTHRGITRPGIYASPVLAASPAASPGIUAARGLEUPRO 144
DB 428 CCGGGAGATCCGTCGGGTCTCACTGCTGGGCGCATGTGACATAGTAAAGCCGCTTCCA 487
QY 145 PROPROPHETPROLEUYSGINVALYLSVALPROILEMETGLUAAMHISILECYASAPALA 164
DB 488 CCGCCATTTCTCTTGAAAGAGGTGAAGGTGCCCATATGAGAAACACACATTTGTGACGCA 547
QY 165 LYETRYHISLEUGLYALATRYTHRGILYASPAAPVALARGILEVALARGASPAEMLEU 184
DB 548 AANATACACCTTGCGGCGCTTACAGGGAGACGACGTCGCGCATGTCGCGTGAAGACATGCTG 607
QY 185 CYEALIGLYASANTHRARGARGSPERCYSGINGIYASPSERGIYGLYPROLEUVALCYB 204
DB 608 TGTGGCGGGAAACCCGAGAGGACCTCATGCCAGGCGCATCCGAGAGGGCCCTGTGTGTC 667
QY 205 LYEVALASNGIYTHRTTRPLEUGINLAGIYVALVASEETRPGIYGLIUGLYCYBALAGIN 224
DB 668 AAGGTGAATGACCTTGCGCTGCGAGGGGGGCGGTGACACTGGGGGAGAGGCTGTGGCCAG 727
QY 225 PROASNAHETPROGIYILETRYTHIRAGVALTHTRYTRYLEUASPTRIEHNHISITYR 244
DB 728 CCCAACCGGCTGGCATCTTACACCGGTGTCACTTACTTGGACTGGATCASCACCTAT 787
QY 245 VALPROLYALYBPRO 249
DB 788 GTCCCAAAAAGCCG 802

RESULT 12
US-10-643-641A-155
: Sequence 155, Application US/10843641A
: Publication No. US20050064454A1
: GENERAL INFORMATION:

```

```

APPLICANT Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OR INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-189
CURRENT APPLICATION NUMBER: US/10/843,641A
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,436
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,832
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/964,824
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/967,768
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR FILING DATE: 2001-10-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: PatentIn version 3.0
SEQ ID NO 155
LENGTH: 1081
TYPE: DNA
ORGANISM: Homo sapiens
US-10-843-641A-155

Alignment Scores:
Pred. No.:      1,75e-155      Length:      1081
Score:          1344.00       Matches:     241
Percent Similarity: 98.37%    Conservative: 0
Best Local Similarity: 98.37% Mismatches:   4
Query Match:     96.48%      Indels:      0
DB:              21         Gaps:        0

US-09-598-982C-21 (1-249) x US-10-843-641A-155 (1-1081)
QY      5   ILeValGlyGngIngIuaIaProArxSerTyvTriProTgInValSerLauArgVal 24
Db      |||
68 ATCTTGAGGGGTCAAGGAGGCCCCAGAGGAAGTGACCTTCGCAGCGTAACCTGAGATC 127
QY      25 HisGIyProTyrTrirPwethIsphAcysGLyGIySerLeuIlleHisProGIntRPValIeu 44
Db      |||
128 CGCACCGCATACTGAGATGACCTTCTGGGGGGCTCCCTATCCACCACCCCGAGGTGCTG 187
QY      45 ThrIaaIaaIacysValIGLyProAspValIyaaspLeuIaaIaleuArgValGlnIeu 64
Db      |||
188 ACCCAACCGCATGCGTGGAGCCGACCGGACGTCAAGGATGTGCCCCCTCAGGGTGCAC 247
QY      65 ArgGlnIHisIeuTyrryrgInaSPGlnLeuIeuProAlserArgIIleIValHis 84
Db      |||
248 CCGGAGAGCACCTCTACTACAGAGACCACTGCTGCGGTACAGCAAGATCATGTGCAC 307
QY      85 ProGlnPherTyThraIagInIlegIyLaASPILeaIaleuIeuGluIeuGluPro 104
Db      |||
308 CCACAGTTCTTACAACCGCCAGATCGAGCGGACATGCGCTGCTGGAGCTGGAGAGCGC 367
QY      105 ValIysValserSerHisValHsrtnValThIeuProProAlaserGluThrPhePro 124
Db      |||
368 GTGAAGGTCTTCCAGCCAGTCCACACCGTCAACCCCTGCCCCCTCAGAGACCTTCCC 427
QY      125 ProGIywerProcSTyTPVaITnGlyTTroGlyASpValaSpbaNaspgIuaTgleuPro 144
Db      |||
428 CCGGGAGATGCCGtGCTGAGTCACTGCTGGGGGAGATGTGACAAATGATGAGCGCTTCCA 487

```

QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
| | | | |
Db 488 CCCCATTTCTCTGAAAGCGGTGAAGGTCCTCCATATGAAAAACACATTTGTGACGCA 547
QY 165 LysTyrHisLeuGlyLysValTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
| | | | |
Db 548 AATATACACCTTGGCCCTTACACGGAGACAGACGTCCGATCTCCGTACACACATGCTG 607
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyLysProLeuValCys 204
| | | | |
Db 608 TGTGCGGGGAAACACCGAGAGGAGCATCTGACAGGCGACCTCCGAGGGCCCTGTGTGC 667
QY 205 LysValAsnGlyThrTrpLysGlnAlaGlyValValSerTrpGlyGlnGlyCysAlaGln 224
| | | | |
Db 668 AAGGTAAATGGACCTGGCTGCGAGCGCGGTGTGCTGAGCTGGGGCCAGGGCTGTGCCAG 727
QY 225 ProAsnArgProGlyLysTyrThrArgValThrTyrTyrLeuAspTrpIleHisIstYr 244
| | | | |
Db 728 CCCAACCGGCTGGCATCTACACCTGTCTACTTACTTGAATCGATCCACCACTAT 787
QY 245 ValProLysLysPro 249
| | | | |
Db 788 GTCCCCAAAAGCCG 802

RESULT 13

US-10-843-641A-714
; Sequence 714, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: Signature Gene Sets
; CURRENT APPLICATION NUMBER: US/10/843,641A
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 714
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-714

Alignment Scores:

Pred. No.: 1,75e-155 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: 21 Gaps: 0

US-09-598-982C-21 (1-249) x US-10-843-641A-714 (1-1081)

QY 5 IleValGlyGlnGlnAlaProArgSerIstYrProTrpGlnValSerIleuArgVal 24
| | | | |
Db 68 ATCGTTGGGGGTCAAGAGGCCCCACAGAGCAAGTGGCCCTGGCAGAGTCAAGTCAAGAGTC 127
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerIleuHisIstYrProGlnTrpValIleu 44
| | | | |
Db 128 CGCGACCGATCTGATGACATTTCTGCGGGGCTCTCTATCCACCCCGAGTGGGTGCTG 187
QY 45 ThrAlaAlaLysValGlyProAspValLysAspLeuAlaLysValGlnLeu 64
| | | | |
Db 188 ACCGACAGGCACTGGTGGGACCGGAGCTCAAGATCTGGCCCTCAGAGTGCACATG 247
QY 65 ArgGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
| | | | |
Db 248 CGGAGACGACCTTACTACACAGACAGCTGCGGCTCAGCAGAGATCATCTGTGAC 307
QY 85 ProGlnPheTyrThrAlaGlnIleGlyLysAlaAspIleAlaLeuGlnLeuGlnIlePro 104
| | | | |
Db 308 CCACAGTTCTACACCGCCAGATCGAGGAGCATGCGCTGTGAGCTGGAGGAGCG 367
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
| | | | |
Db 368 GTGAAGTCTCCAGCCAGCTCCACAGGTCACCTGCCCCCTGCTCAGAGCTTCCCC 427
QY 125 ProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAspGluArgLeuPro 144
| | | | |
Db 428 CCGGGGATGCGCTGTGGGTCACTGGCTGGGCGATGTGGACATAGATGAGCGCTCCCA 487
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
| | | | |
Db 488 CCCCATTTCTCTGAAAGCGGTGAAGTCCCATTAAGAAACACATTTGTGACGCA 547
QY 165 LysTyrHisLeuGlyLysValTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
| | | | |
Db 548 AATATACACCTTGGCCCTTACACGGAGACAGACGTCCGATCTCCGTACACACATGCTG 607
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyLysProLeuValCys 204
| | | | |
Db 608 TGTGCGGGGAAACACCGAGAGGAGCATCTGACAGGCGACCTCCGAGGGCCCTGTGTGC 667
QY 205 LysValAsnGlyThrTrpLysGlnAlaGlyValValSerTrpGlyGlnGlyCysAlaGln 224
| | | | |
Db 668 AAGGTAAATGGACCTGGCTGCGAGCGCGGTGTGCTGAGCTGGGGCCAGGGCTGTGCCAG 727
QY 225 ProAsnArgProGlyLysTyrThrArgValThrTyrTyrLeuAspTrpIleHisIstYr 244
| | | | |
Db 728 CCCAACCGGCTGGCATCTACACCTGTCTACTTACTTGAATCGATCCACCACTAT 787
QY 245 ValProLysLysPro 249
| | | | |
Db 788 GTCCCCAAAAGCCG 802

RESULT 14

US-10-843-641A-5153
; Sequence 5153, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: Signature Gene Sets
; CURRENT APPLICATION NUMBER: US/10/843,641A
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832

Qy	225	ProAnaAaRProGlyIleTyrThrArgValThrTyrTyrIleuAspTPIleHisIcTyr	244
Db	728	CCCAACGGCGCTGGGATCTACACCGGTGCACTGACTGACTGATCCACCACTAT	78
Qy	245	ValProLYsLYsPro 249	
Db	788	GTCCCAAAAAGCCG 802	
	RESULT 15		
	US-10-275-505-27		
	Sequence 27, Application US/10275505		
	Publication No. US20040081961A1		
	GENERAL INFORMATION:		
	APPLICANT: INCYTE GENOMICS, INC.		
	APPLICANT: DELBEANE, Angelo M.; LAL, Preeti G.		
	APPLICANT: HAFALIA, April U.A.; PATTERSON, Chandra		
	APPLICANT: WALIA, Naxinder K.; KEANEY, Liam		
	APPLICANT: TRIBOLEY, Catherine M.; KHAN, Farrah A.		
	APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.		
	APPLICANT: AZIMZAI, Valda; ELIOTT, Vicki S.		
	APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.		
	APPLICANT: YANG, Junming; HERNANDEZ, Roberto		
	APPLICANT: POLICKY, Jennifer L.; LU, Dyrung Anna M.		
	APPLICANT: REDDY, Roopa M.; YUE, Henry		
	APPLICANT: TANG, Y. Tom		
	TITLE OF INVENTION: PROTEASES		
	FILE REFERENCE: PI-0085 USN		
	CURRENT APPLICATION NUMBER: US/10/275, 505		
	CURRENT FILING DATE: 2002-11-04		
	PRIOR APPLICATION NUMBER: PCT/US01/14651		
	PRIOR FILING DATE: 2001-05-04		
	PRIOR APPLICATION NUMBER: 60/209, 402		
	PRIOR FILING DATE: 2000-06-01		
	PRIOR APPLICATION NUMBER: 60/207, 477		
	PRIOR FILING DATE: 2000-05-25		
	PRIOR APPLICATION NUMBER: 60/205, 803		
	PRIOR FILING DATE: 2000-05-17		
	PRIOR APPLICATION NUMBER: 60/203, 566		
	PRIOR FILING DATE: 2000-05-11		
	PRIOR APPLICATION NUMBER: 60/202, 082		
	PRIOR FILING DATE: 2000-05-04		
	NUMBER OF SEQ ID NOS: 28		
	SOFTWARE: PERL Program		
	SEQ ID NO 27		
	LENGTH: 2662		
	TYPE: DNA		
	ORGANISM: Homo sapiens		
	FEATURE:		
	NAME/KEY: misc feature		
	OTHER INFORMATION: Incyte ID No: 7472460CB1		
	US-10-275-505-27		
	Alignment Scores:		
	Pred. No.:	4,13e-153	Length: 2662
	Score:	1329.00	Matches: 238
	Percent Similarity:	97.14%	Conservative: 0
	Best Local Similarity:	97.14%	Mismatches: 7
	Query Match:	95.41%	Indels: 0
	DB:	18	Gaps: 0
	US-09-598-982C-21 (1-249) x US-10-275-505-27 (1-2662)		
Qy	5	IlleValIGlyGlnGluAlaProArgserIySTPrPOTPGIValIsertIeuArgVal	24
Db	701	ATCTGTGGGGGATCAAGAGGCCCCCGAGGAGCAAGTGGCCCTGGGCAAGTGAAGCTC	760
Qy	25	HisGlyProTyrTTrMetHisIspHeCysGlyGlySerIleuIleHisProGIntPrValIleu	44
Db	761	CGGAGCCAGTATGAGATGCACTTCGGCGGGGCTCCCTCATCCACCCCGAGTGGTCTG	820
Qy	45	ThrAlaAlaAlaCysValIGlyProAspValIyAspIleuAlaAlaIeuArgValGlnIleu	64

Db 821 ACCGACGCCACTGCGTGGGACCGGACGTCAGAGATCTGGCCGCTCAAGGTCAACTG 880
QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
Db 881 CCGGACGACGACTCTACTACGACGACGACGACGCTGCTGCCGTGACGAGATCATCGTGAC 940
QY 85 ProGlnPheTyrThrIleGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
Db 941 CCACAGTTCTACACCCGCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 1000
QY 105 ValIleValSerSerHisValHisThrValThrLeuProProAlaSerGlnThrPhePro 124
Db 1001 GTCAAGCTCTCCAGCCACGTCACAGGTCACCTGCCCTGCTCAAGACCTTCCCC 1060
QY 125 ProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAspGluArgLeuPro 144
Db 1061 CCGGGGATGCCGCTGGGTCACTGGCTGGGGGATGTGGACATGATGAGGCGCTCCCA 1120
QY 145 ProProPheProLeuLeuGlnValIleValProIleMetGluAsnHisIleCysAspAla 164
Db 1121 CCGCCATTTCCTCTGAAGCATGTGAAGTCCCATATGGAACCAACATTTGTGACGCA 1180
QY 165 LysTyrHisLeuGlyValIleTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
Db 1181 AATATCACCTTGCGCGCTACACGAGAGACGACGTCGCCATCGTCCGTGACGACATGCTG 1240
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 1241 TGTGCCGGGAAACCCGGAGGAGCTCATGCGAGGGGCACTCCGGAGGGCCCTGGGTGTC 1300
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValIleValSerTrpGlyGluGlyCysAlaGln 224
Db 1301 AAGGTGAATGGCACCTGCTGCGACGGCGGCGTGTCAATGGGAGAGGGCTGTGCCAG 1360
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrpIleHisIleTyr 244
Db 1361 CCCAACCGGCTGGCATCTACACCCGTGTCACTACTTGAGCTGATCCACCACTAT 1420
QY 245 ValProIleLysPro 249
Db 1421 GTCCCCAAAAGCCG 1435

Search completed: August 27, 2005, 23:11:52
Job time : 613 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 27, 2005, 19:35:09 ; Search time 178 Seconds

(without alignments)
2288.949 Million cell updates/sec

Title: US-09-598-982c-21

Perfect score: 1393
Sequence: 1 LEKRVGGGEARSRKMPQV.....ITYRTVYLDVIMHVPKKP 249

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xip
-O=/cgn2_1/USPTO.spool.p/US09598982/rnuc 25082005.165518.269/app.query.fasta_1.391
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rxn1 -MINMATCH=0.1 -LOOPECL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=humand40.cdi
-LIST=45 -DOCATLGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09598982@cgn1_1.105 @runat 25082005.165518.269 -NCPU=6 -ICPU=3
-NO WMAP -LARGEOBQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	99.6	771	3	US-09-079-970A-4
2	1368	98.2	735	3	US-09-079-970A-1
3	1368	98.2	1128	2	US-09-016-366A-20
4	1368	98.2	1128	2	US-08-978-404B-15
5	1363	97.8	1137	2	US-09-016-366A-18
6	1363	97.8	1137	2	US-08-978-404B-13
7	1344	96.5	1081	2	US-09-016-366A-22
8	1344	96.5	1081	2	US-08-978-404B-17
9	1344	96.5	1081	4	US-09-917-254-50
10	1274	91.5	1154	2	US-09-016-366A-16
11	1274	91.5	1154	2	US-08-978-404B-11
12	1091	78.3	1108	2	US-09-016-366A-14

13	1091	78.3	1108	2	US-08-978-404B-20	Sequence 20, Appl
14	1075	77.2	1219	2	US-08-978-404B-7	Sequence 7, Appl
15	1054	75.7	1031	2	US-08-978-404B-1	Sequence 1, Appl
16	1051	75.4	1097	2	US-08-978-404B-4	Sequence 4, Appl
17	1051	75.4	1103	2	US-09-016-366A-24	Sequence 24, Appl
18	1000.5	71.8	2259	2	US-08-845-998-3	Sequence 3, Appl
19	1000.5	71.8	2259	3	US-09-206-537-3	Sequence 3, Appl
20	1000.5	71.8	2259	3	US-09-430-854-3	Sequence 3, Appl
21	979	70.3	3757	2	US-09-016-366A-13	Sequence 13, Appl
22	979	70.3	3757	2	US-08-978-404B-19	Sequence 19, Appl
23	961.5	69.0	2218	2	US-08-845-998-5	Sequence 5, Appl
24	961.5	69.0	2218	3	US-09-206-537-5	Sequence 5, Appl
25	961.5	69.0	2218	3	US-09-430-854-5	Sequence 5, Appl
26	836.5	60.1	2397	2	US-08-978-404B-2	Sequence 2, Appl
27	836.5	49.1	1095	2	US-08-978-404B-9	Sequence 9, Appl
28	563.5	40.5	980	4	US-09-023-942A-30	Sequence 30, Appl
29	563.5	40.5	1110	3	US-09-386-653A-1	Sequence 1, Appl
30	561.5	40.3	1212	4	US-09-620-312D-431	Sequence 431, App
31	554.5	39.8	1130	4	US-09-386-653A-8	Sequence 8, Appl
32	552	39.6	933	4	US-09-023-942A-29	Sequence 29, Appl
33	536.5	38.5	1613	4	US-09-387-375-1	Sequence 1, Appl
34	536.5	38.5	1613	4	US-10-041-400A-1	Sequence 1, Appl
35	536.5	38.5	1613	4	US-10-042-091A-1	Sequence 1, Appl
36	527.5	37.9	1130	4	US-09-387-375-8	Sequence 8, Appl
37	527.5	37.9	1130	4	US-10-041-400A-8	Sequence 8, Appl
38	527.5	37.9	1130	4	US-10-042-091A-8	Sequence 8, Appl
39	507	36.4	1142	3	US-09-386-642-8	Sequence 8, Appl
40	507	36.4	1169	3	US-09-386-642-7	Sequence 7, Appl
41	501.5	36.0	1165	4	US-09-023-942A-28	Sequence 28, App
42	501.5	36.0	1378	4	US-09-907-794A-262	Sequence 262, App
43	501.5	36.0	1378	4	US-09-905-125A-262	Sequence 262, App
44	501.5	36.0	1378	4	US-09-902-775A-262	Sequence 262, App
45	501.5	36.0	1378	4	US-09-906-700-262	Sequence 262, App

ALIGNMENTS

RESULT 1
US-09-079-970A-4
; Sequence 4, Application US/09079970A
; Patent No. 6274366
; GENERAL INFORMATION:
; APPLICANT: Mafilt, Mark A.
; APPLICANT: Miles, Andrew L.
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: Enzymatically-Active Recombinant Human
; TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Intellectual Property Department
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,970A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506, 073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; US-09-079-970A-4

```
/
/ LENGTH: 771 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 7..753
/
/ FEATURE:
/ NAME/KEY: misc signal
/ LOCATION: 7..18
/
US-09-079-970A-4

Alignment Scores:
Pred. No.: 3,11e-150 Length: 771
Score: 1387.00 Matches: 248
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 99.57% Indels: 0
DB: 3 Gaps: 0

US-09-598-982c-21 (1-249) x US-09-079-970A-4 (1-771)
QY 1 LeuGluLysArgIleValGlyGlnGluAlaProArgSerIleTTPProTglnVal 20
Db 7 CTGGAAGAAAGATCGTCGGGGGTCAAGAGCCCGGAGCAAGTGGCTGGAGGTG 66
QY 21 SerLeuArgValHisGlyProTyrTTPMetHisPheCysGlyGlySerLeuIleHisPro 40
Db 67 AGCTTGAAGTCCACCGCCCATCTGATGCACTTCTGGGGGGGCTCCCTCATCCACCC 126
QY 41 GlnTTPValLeuThrAlaAlaCysValGlyProAspValIleAspLeuAlaLeu 60
Db 127 CAGTGGGTGTGTCGCGAGGCACTCGTGGGCGGAGCAAGATCTGGCGGCTTC 186
QY 61 ArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
Db 187 AGGTGTCAATCGCGGAGGAGGACGCTCTACTACAGACAGAGTGTGCGGTGAGGAG 246
QY 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGln 100
Db 247 ATCATGTGCACCCACAGATTCTACCGGCGGAGATGAGGAGGACATCCGCTGTGAG 306
QY 101 LeuGluGlnProValLysValSerSerHisValHisThrValThrLeuProAlaSer 120
Db 307 CTGGAGAGCGGATGAAGGTCTTCACCGCACGTCACACGATCCCTGCCCCGCTCA 366
QY 121 GlnThrPheProGlnPheProCysTTPValThrGlyTTPGlyAspValAspAsp 140
Db 367 GAGACCTTCCCCCGGGGATGCGGTCTGGTCACTGGGCGCATGTGACATATGAT 426
QY 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
Db 427 GAGCGCTTCCACCGCATTTCTCTGAAGCAGGTGAAGTCCCATATGAAAAACAC 486
QY 161 IleCysAspAlaIleTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180
Db 487 ATTGTGAGCAAAATACCACTTGGCGCTACACGAGAGACGATCCGCAATCGCTCT 546
QY 181 AspAspMetLeuCysAlaGlnAsnThrArgAspSerCysGlnGlyAspSerGlyGly 200
Db 547 GACGATATCTGTGTCCGGGAAACACCGGAGGGAATCTGCAAGGCGCATCCGAGGG 606
QY 201 ProLeuValCysLysValAsnGlyThrTTPLeuGlnAlaGlyValValSerTTPGlyGln 220
Db 607 CCCCTGGGTGTGCAAGGTGATGCACTGTGCGAGGCGGCGTGTGAGTGGGCGAG 666
QY 221 GlyCysAlaGlnProAspArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTTP 240
```

```
Db 667 GGCTGTGCCACCGCCAGCGGCTGAGCATCTACACCGGTGTCACTTGTGACTGG 726
QY 241 IleHisIleTyrValProLysIlePro 249
Db 727 ATTCACACTATGTCTCCCAAAAGCCG 753

RESULT 2
US-09-079-970A-1
/ Sequence 1, Application US/09079970A
/ Patent No. 6274366
/
/ GENERAL INFORMATION:
/ APPLICANT: Mallitc, Mark A.
/ APPLICANT: Niles, Andrew L.
/ APPLICANT: Haak-Frendscho, Mary
/ TITLE OF INVENTION: Enzymatically-Active Recombinant Human
/ TITLE OF INVENTION: Beta-Trypsin and Method of Making Same
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Intellectual Property Department
/ STREET: 8000 Excelsior Drive, Suite 401
/ CITY: Madison
/ STATE: WISCONSIN
/ COUNTRY: U.S.A.
/ ZIP: 53717-1914
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/079, 970A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Leone, Joseph T.
/ REGISTRATION NUMBER: 37,170
/ REFERENCE/DOCKET NUMBER: 34506.073
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 831-2100
/ TELEFAX: (608) 831-2106
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 735 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..735
/
US-09-079-970A-1

Alignment Scores:
Pred. No.: 4.49e-148 Length: 735
Score: 1368.00 Matches: 244
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 98.21% Indels: 0
DB: 3 Gaps: 0

US-09-598-982c-21 (1-249) x US-09-079-970A-1 (1-735)
QY 5 IleValGlyGlnGlnAlaProArgSerIleTTPProTglnValSerLeuArgVal 24
Db 1 ATCGTCGGGGGTCAAGAGGCGCCAGAGCAAGTGGCCCTGGAGGTGAGGATC 60
QY 25 HisGlyProTyrTTPMetHisPheCysGlyGlySerLeuIleHisProGlnTTPValLeu 44
Db 61 CACGCGCATACTGATGCACTTCTGCGGGGGCTCCCTCATCCACCCGAGTGGTCTG 120
```

QY 45 ThrAlaAlaAlaCysValGlyProAspValIlysaAspLeuAlaAlaLeuArgValGlnLeu 64
DB 121 ACCGAGGCGACTGGTGGGACCGGACGTCAGAGATCTGGCCGCTCAGGGTGGACCTG 180
QY 65 ArgGlnGlnIleLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
DB 181 CCGGAGCAGCACTTACTACCAAGACCAAGCTGCTGCGGTGACAGATCATCTGTGCAC 240
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlnLeuGlnPro 104
DB 241 CCACAGTCTTACACCGCCAGATCGAGCGACATCGCCCTCTGAGCTGAGAGAGCCG 300
QY 105 ValIlysaIleSerSerHisValHisThrValThrLeuProProAlaSerGlyThrPhePro 124
DB 301 GTGAAGGCTCTCCAGCCAGCTCCACCGCTCACCCCTGCTCCCTCAGAGACCTTCCC 360
QY 125 ProGlyMetProCysTyrValThrGlyTyrGlyAspValAspAsnAspGlyuArgLeuPro 144
DB 361 CCGGGGATGCTGCTGGGTCTGCTGCTGGGCGCATGTGACAAATGATGAGGCTCCCA 420
QY 145 ProProPheProLeuIlysaGlnValIlysaValProIleMetGluAsnHisIleCysAspAla 164
DB 421 CCGCATTTCTCTGAGAGAGGTGAAGGTCCCATTAATGAAAAACCATTTGTGACGCA 480
QY 165 LysTyrHisIleLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
DB 481 AAATACCACTTGGGCTGCTCACCGGAGACGACGTCCTGCTGCTGACCAACATGCTG 540
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyIlyProLeuValCys 204
DB 541 TGTGCGGGAGACACCGGAGGACTCATTCACGGGCGACTCCGGAGGGCCCTGCTGTGC 600
QY 205 LysValAsnGlyThrTyrLeuGlnAlaGlyValIlysaIleSerTyrGlyGlnGlyCysAlaGln 224
DB 601 AAGTGAAATGGACCTGGCTGCGAGCGGGCGTGTCACTGGGGCGAGGGCTGTGCCAG 660
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTyrIleHisIleTyr 244
DB 661 CCCAACCGGCTGGGATCTACACCGGTGTCACTTACTTGAGTGTGATCCACCATAT 720
QY 245 ValProIlysaIlysaPro 249
DB 721 GTCCCCAAAAGCCG 735

RESULT 3
US-09-016-366A-20
; Sequence 20, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090

; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-016-366A-20
Alignment Scores:
Pred. No.: 8,696-148 Length: 1128
Score: 1368.00 Matches: 244
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 98.21% Indels: 0
DB: 2 Gaps: 0
US-09-598-982C-21 (1-249) x US-09-016-366A-20 (1-1128)
QY 5 ILevalGlyGlnGlnAlaProAspSerIlyTyrProTyrGlnValSerLeuArgVal 24
DB 89 ATCGTGGGGGTGACAGAGGCCCCAGAGAGCAATGGCCCTGAGAGCTGAGAGCTC 148
QY 25 HisGlyProTyrTyrMetHisPheCysGlyGlySerLeuIleHisProGlnTyrValLeu 44
DB 149 CACGGCCCATCTGGAATGCACTTCTGCGGGGCTCCCTCATCCACCCCAATGGGTGCTG 208
QY 45 ThrAlaAlaAlaCysValGlyProAspValIlysaAspLeuAlaAlaLeuArgValGlnLeu 64
DB 209 ACCGAGGCGACTGGGTGGACCGGACGTCAAGGATCTGGCCGCTCAGAGGTGCACTG 268
QY 65 ArgGlnGlnIleLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
DB 269 CCGGAGCAGCACTCTTACTACAGGACCAAGCTGTGCGGTCAGAGGATCATGCTGCAC 328
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlnLeuGlnPro 104
DB 329 CCACAGTCTTACACCGCCAGATCGAGCGGACATCGCTGCTGGAGCTGAGAGAGCCG 388
QY 105 ValIlysaIleSerSerHisValHisThrValThrLeuProProAlaSerGlyThrPhePro 124
DB 389 GTGAAGTCTCCAGCCAGCTCCACAGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
QY 125 ProGlyMetProCysTyrValThrGlyTyrGlyAspValAspAsnAspGlyuArgLeuPro 144
DB 449 CCGGGGATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 508
QY 145 ProProPheProLeuIlysaGlnValIlysaValProIleMetGluAsnHisIleCysAspAla 164
DB 509 CCGCATTTCTCTGAGAGCAGGTGAAGGTCCCATTAATGAAAAACCATTTGTGACGCA 568
QY 165 LysTyrHisIleLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
DB 569 AAATACCACTTGGGCTTACACCGGAGACAGATCGCCGATCTGCTGAGAGCATGCTG 628
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyIlyProLeuValCys 204
DB 629 TGTGCGGGAGACACCGGAGGACTCATGCAAGGCGCACTCCGAGGGCCCTGCTGTGC 688
QY 205 LysValAsnGlyThrTyrLeuGlnAlaGlyValIlysaIleSerTyrGlyGlnGlyCysAlaGln 224
DB 689 AAGTGAAATGGACCTGGCTGCGAGCGGCGTGTGTCACTGGGCGAGAGGCTGTGCCAG 748
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTyrIleHisIleTyr 244

Db 749 CCAACCGGCTGGCATCTACACCCGCTGACCTACTGAGATCCACCACTAT 808
Qy 245 ValProlylsylsPro 249
Db 809 GTCCCCAAAAGCCG 823

RESULT 4

US-08-978-404B-15

Sequence 15, Application US/08978404B

Patent No. 5968782

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES

NUMBER OF INVENTION: FIBRINOGEN

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,404B

FILING DATE: 25-NOV-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032,354

FILING DATE: 04-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7090

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 1128 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-978-404B-15

Alignment Scores:

Pred. No.: 8,69e-148 Length: 1128

Score: 1368.00 Matches: 244

Percent Similarity: 99.59% Conservativity: 0

Best Local Similarity: 99.59% Mismatches: 1

Query Match: 98.21% Indels: 0

DB: 2 Gaps: 0

US-09-598-982C-21 (1-249) x US-08-978-404B-15 (1-1128)

Qy 5 l1evalgylgylnglualaproatgserlystiprictipglnvalserleuargval 24
Db 89 ATCGTGGGGGTGACAGAGGCCCCAGAGCAAGTGGCCCTGAGAGTGCCTGAGAGTC 148
Qy 25 Hsaglyprrtyrtrmehisphesysylgylserleu1ehisproglintrryvalleu 44
Db 149 CACGGCCACTACTGATGACCTTCTGCGGGGCTCCCTATCCACCCAGTGGGTGCTG 208
Qy 45 Thr1aalaa1acyvalgylproaspvallyasplleu1aalaleuargvalglnleu 64
Db 209 ACCGAGCGCCACTGCTGGGACCGGACGTCGAAGATCTGGCCGCTCGAGGTGCACTG 268

Qy 65 ArggluglnhisleuTyrrTglnaspGlnleuProvalSerArglle1valhis 84
Db 269 CGGAGACGACACTTACTATACAGGACGAGCTGCGCGGTACAGAGATCATCTGCAC 328
Qy 85 ProglinphetyrrTthAlaglnlleGlylaaaprllealaleuGlnleuGlnleu 104
Db 329 CCACAGTTCTACACCCGCAATGAGAGGACATGCTGCTGAGACTGAGAGGACCG 388
Qy 105 VallysValSerSerhisValhisThrValThrleuProProalaserGluThrPhePro 124
Db 389 GTGAAGGCTCTCAGGACGACGTCACACGCTCACCTGCCCTGCTCAGAGACTTCCCC 448
Qy 125 ProglimeProCystrpValThrGlyTrpGlyaspValaaspamaspGlnargleuPro 144
Db 449 CCGGGGATGCGGTGCTGGGTGCTGCTGCGGGGCGATGGGACAAATGATGAGCGCTCCCA 508
Qy 145 PropropheProleu1eulVallyValProilemetGluAanHis1leCyaspAla 164
Db 509 CCGCATTTCTCTGACAGGTGAAAGTCCCCATATGAAACACATTTGTGACGCA 568
Qy 165 LysTyrrhisleuGlyAlaTyrrThrGlyaspaspValargilevalargaspaspleu 184
Db 569 AAATACACCTTGGGCGCTTACACGGGAGACGACGTCGCTGTCGAGACATGCTG 628
Qy 185 CybalaglyAenThrArgArgaspserCyglnglyaspserGlylyProleuValys 204
Db 629 TGTGCGGGAAACACCCGAGGAGACTCATGACAGGCGCATCCGAGGGCCCTGTGTGC 688
Qy 205 LysValaaspGlyThrTrpleuGlnalaglyValValaserTpGlyGlnGlyCybalagln 224
Db 689 AAGGTGAATGGACCTGCTGCTGACGGGCGGTGCTGCTGAGGGGCGAGGCTGTGCCAG 748
Qy 225 ProbanargProgllyleTyrrThrArgValThrTyrrleuaspTrp1ehis1eTyrr 244
Db 749 CCAACCGGCGCTGGATCTACACCGGTGTCACTACTGACTGATCCACCATAT 808
Qy 245 ValProlylsylsPro 249
Db 809 GTCCCCAAAAGCCG 823

RESULT 5

US-09-016-366A-18

Sequence 18, Application US/09016366A

Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,366A

FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,090

FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7093

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1137 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-016-366A-18

Alignment Scores:
 Pred. No.: 3,32e-147 Length: 1137
 Score: 1363.00 Matches: 243
 Percent Similarity: 99.18% Conservative: 0
 Best Local Similarity: 99.18% Mismatches: 2
 Query Match: 97.85% Indels: 0
 Gaps: 0

US-09-598-982C-21 (1-249) x US-09-016-366A-18 (1-1137)

```

OY 5 11eValG1yG1ng1ua1aProArGserLySTrPProTgInVa1SerLeuArGVal 24
Db 87 ATCGTCGGGGGTCAAGAGGCCGCCAGAGCAAGTGGCTGGCAGTGAAGCTC 146
OY 25 H1sG1pProTyTTrPMeth1sPheCySg1yG1ySerLeu1eH1sProG1nTrValleu 44
Db 147 CACGGCCCATCTGATGATGACTTCTGCGGGGGCTCCCTCATCACCCCAAGTGGTGTG 206
OY 45 Thr1a1a1a1aCyVa1G1yProArVa1LyAsPleuA1a1a1euaArG1n1eua 64
Db 207 ACCGAGCGCACTGGTGGAGCCGAGCGCAAGATCTGGCCGCTCAAGGTGCACTG 266
OY 65 ArgG1nG1nH1sLeuTyTTrG1nAsP1nLeuProVa1SerArg11e1eValH1s 84
Db 267 CCGAGAGCAAGCACTCTACTACAGAGCAAGCTGCTGCGCTGAGCAAGATCATCTGTGCA 326
OY 85 ProG1nPhyTyTThrAlaG1n11eG1yAlaAsP11eAlaLeuG1n1euaG1n1eua 104
Db 327 CCACAGTTCTACACCGCCAGATCCGAGCGGACATCGCTGCTGAGCTGAGAGCGCG 386
OY 105 ValLyVa1SerSerH1eValH1sThrVal1ThrLeuProAr1a1SerG1uThrPhePro 124
Db 387 GTAAAGCTCTCAAGCAAGTCAACAGCTGACCTGCCCCCTCAGAGACTTTCGCC 446
OY 125 ProG1yMetProCySTrPVal1ThrG1yTrP1yAsPVal1AsPAsnAsP1uArG1euaPro 144
Db 447 CCGGGGATGCCCTGCTGGGTCACTGGCTGGGCGCATGTGCAATGATGAGGCGCTCCCA 506
OY 145 ProPheProLeuLySg1nValLyVa1Pro11eMetG1uAsnH1s11eCyAsPAla 164
Db 507 CCGCCATTTCCTCTGAGAGCGGTGAAGGTCCCATTAATGAAACCACTTTGTGACCA 566
OY 165 LySTrH1sLeuG1yAlaTyTThrG1yAsPArVa1ArG11eVal1ArGAsPAsn1eLeu 184
Db 567 AAATACCACTTGGGCTGACAGGAGAGCAAGCTGCGCATGTCCGAGCAAGATGCTG 626
OY 185 CySa1aG1yAsnThrArgArGAsPserCySg1nG1yAsPserG1yG1yProLeuVal1CyS 204
Db 627 TGTGCGGGAGACACCCGAGAGGACTCATGCCAGGGCGACTCCGAGGGGCCCTGTGTGTC 686
OY 205 LyVa1a1euaG1yThrTrP1euaG1n1aG1yAla1Val1SerTrP1yG1nG1yCySa1aG1n 224
Db 687 AAGGTGAATGCACTGCTGAGAGGCGGCGGTGACGCTGGGGGAGAGGCTGTCCAG 746
OY 225 ProAsnArGProG1y11eTyTThrArGVal1ThrTyTTrLeuAsPTr11eH1s1eTyT 244
Db 747 CCAACCGGCTGGCATCTACACCGGTGCTCACTACTACTGAGCTGAGATCAACACATAT 806
OY 245 ValProLyVa1ySPro 249
  
```

Db 807 GTCCCAAAAAGCCG 821

RESULT 6
 US-08-978-404B-13
 Sequence 13, Application US/08978404B
 Patent No. 5968782
 GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 TITLE OF INVENTION: FIBRINOGEN
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P. C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,404B
 FILING DATE: 25-NOV-97
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,354
 FILING DATE: 04-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7090
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1137 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-978-404B-13

Alignment Scores:
 Pred. No.: 3,32e-147 Length: 1137
 Score: 1363.00 Matches: 243
 Percent Similarity: 99.18% Conservative: 0
 Best Local Similarity: 99.18% Mismatches: 2
 Query Match: 97.85% Indels: 0
 Gaps: 0

US-09-598-982C-21 (1-249) x US-08-978-404B-13 (1-1137)

```

OY 5 11eValG1yG1ng1ua1aProArGserLySTrPProTgInVa1SerLeuArGVal 24
Db 87 ATCGTCGGGGGTCAAGAGGCCGCCAGAGCAAGTGGCTGGCAGTGAAGCTC 146
OY 25 H1sG1pProTyTTrPMeth1sPheCySg1yG1ySerLeu1eH1sProG1nTrValleu 44
Db 147 CACGGCCCATCTGATGATGACTTCTGCGGGGGCTCCCTCATCACCCCAAGTGGTGTG 206
OY 45 Thr1a1a1a1aCyVa1G1yProArVa1LyAsPleuA1a1a1euaArG1n1eua 64
Db 207 ACCGAGCGCACTGGTGGAGCCGAGCGCAAGATCTGGCCGCTCAAGGTGCAACTG 266
OY 65 ArgG1nG1nH1sLeuTyTTrG1nAsP1nLeuProVa1SerArg11e1eValH1s 84
Db 267 CCGAGAGCAAGCACTCTACTACAGAGCAAGCTGCTGCGGTCAGAGATATCTGTGAC 326
OY 85 ProG1nPhyTyTThrAlaG1n11eG1yAlaAsP11eAlaLeuG1n1euaG1n1eua 104
  
```

```

Db      327 CCACAGTTCTACACCCGCCAGATCGAGCGGACATGCCCTGTGAGCTGGAGGCGCG
Qy      105 VallyValSerSerHisValHisThrValThreProProHisSerGluThrPhePro
Db      387 GTGAAGCTCTCCAGCCACGCTCCACAGGTCACCTGCCCTGCTCCAGAGACCTTCCCC
Qy      125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValArgIleValArgAspMetLeu
Db      447 CCGGGATGCGCGTGGGTCACTGGCTGGGGGATGTGGACATGATGATGAGCGCTCCCA
Qy      145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla
Db      507 CCGCCATTCTCTTGAGAGAGGTGAAGTCCCATATGAAAACCACTTTGTGACGA
Qy      165 LysTyrHisLeuGlyValAlaTyrThrGlyAspAspValArgIleValArgAspMetLeu
Db      567 AATATACCACTTGGCCCTCAACGAGAGACGATCCGATGCTCCGTACAGACATGCTG
Qy      185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
Db      627 TGTGCGGGGAACCCGAGGAGCATCATGCAAGGCGACTCCGAGAGGCCCCGTGGTGTG
Qy      205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlnGlyCysAlaGln
Db      687 AAGGTAAATGGACCTGGCTGACGAGCGGCGTGTGAGCTGGGCGAGGCGTGTGCCAG
Qy      225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisIleTyr
Db      747 CCAACCGGCGTGGCATCTACACCCGTGTCACTTACTTGAATCGATCCACCACTAT
Qy      245 ValProLysLysPro 249
Db      807 GTCCCCAAAAAGCCG 821

RESULT 7
US-09-016-366A-22
; Sequence 22, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1081 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-016-366A-22

Alignment Scores:
Pred. No.: 4,76e-145 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: 2 Gaps: 0

US-09-598-982C-21 (1-249) x US-09-016-366A-22 (1-1081)

Qy      5 ILeValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db      68 ATCGTTGGGGGTCAAGAGCCGCCAGAGCAAGTGCCCTGGCAGGTGAGCTGAGAGTTC 127
Qy      25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
Db      128 CCGGACCGATCTGATGATGACTTCTGCGAGGAGCTCTCATATCCACCCCACTGGAGTCTG 187
Qy      45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
Db      188 ACCGACGACGACTGCGTGGAGACCGGACGTCAGAGATCTGGCCGCTCAGGAGTGCACCTG 247
Qy      65 ArgGlnGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleIleValHis 84
Db      248 CCGGAGCAGCACTTACTTACACGAGCAGCTGCTGCGGTCAAGAGATCATCGTGCAC 307
Qy      85 ProGlnPheTyrThrAlaGlnIleGlyValAspIleAlaLeuGlnLeuGluPro 104
Db      308 CCACAGTTCTACACCGCCCAATCCGAGCGAGACATCGCTGCTGAGACTGAGAGACCTG 367
Qy      105 VallyValSerSerHisValHisThrValThreProProHisSerGluThrPhePro 124
Db      368 GTGAAGCTCTCCAGCCACGCTCCACAGGTCACCTGCCCTGCTCAGAGACCTTCCCC 427
Qy      125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspGluArgLeuPro 144
Db      428 CCGGGATGCGCGTGGGTCACTGCTGGGCGCATGTGGAACAATGATGAGGCGCTCCCA 487
Qy      145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db      488 CCGCATTTCTCTTAAAGCAGGTGAAGTCCCATATGAAACCAACATTTGTGACGCA 547
Qy      165 LysTyrHisLeuGlyValAlaTyrThrGlyAspAspValArgIleValArgAspMetLeu 184
Db      548 AATATACCACTTGGCGCTTACACGAGGAGACGATCCGATGTCGTGAGACATGCTG 607
Qy      185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db      608 TGTGCGGGGAACACCCGAGGAGCATCATGCAAGGCGACTCCGAGGCGCCCTGTGTGC 667
Qy      205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlnGlyCysAlaGln 224
Db      668 AAGGTAAATGGACCTTGGCTGACGAGCGGCGGTGTGCTGAGTGGGGGAGGCTGTGCCAG 727
Qy      225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisIleTyr 244
Db      728 CCAACCGGCGCTGGGATCTACACCGGTGTCACTTACTTGAATGATGATCACCACATAT 787
Qy      245 ValProLysLysPro 249
Db      788 GTCCCCAAAAAGCCG 802

RESULT 8
US-08-978-404B-17
; Sequence 17, Application US/08978404B

```

Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Discrete
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-17
Alignment Scores:
Pred. No.: 4,766-145 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
Gaps: 0
US-09-598-982c-21 (1-249) x US-08-978-404B-17 (1-1081)
QY 5 l l e v a l g i y g l i n g l u a l a p r o a r g s e r l y t r p r o t r p g l i n v a l s e r l e u a r g v a l 24
DB 68 a t c g t t g g g g g t c a g a g g c c c c a g a g a c a g t g c c t t g c a g a g t g a c t g a g a g t c 127
QY 25 h i s g l y p r o t y r t r p m e t h i s p h e c y s g l y s e r l e u l l e h i s p r o g l i n t r p v a l l e u 44
DB 128 c g c g a c c a g t a c t g a t g a c a t t c t g c g g g g c t c c t c a t c a c c c a c a g g g t g a t g t g 187
QY 45 t h r l a a l a a l a c y s v a l g l y p r o a s p v a l l y s a s p l e u a l a l e u a r g v a l g l n l e u 64
DB 188 a c c g a c c a g c a c t g c t g g g a c c g a c g t c a g a g a t c t g g c c c t t c a g g g t g c a a c t g 247
QY 65 a r g l i n g l i n h i s l e u t y r t r g l n a s p g l n l e u p r o v a l s e r a r g l l e l l e v a l h i s 84
DB 248 c g g a g a c a g a c c t a c t a c c a g a c a g c g t g c g g t c a g a g a t c a t c g t g c a c 307
QY 85 p r o g l i n p h e t y r t h r l a g l i n l l e g l y a l a a s p l l e a l e u l e u g l i n l e u g l i n u p r o 104
DB 308 c c a c a g t t c t a c a c c g c c a g a t c g a g a g a c a t c g c t g a g a g t g a g a g c g 367
QY 105 v a l l y s a l s e r s e r h i s v a l h i s t h r v a l t h r l e u p r o a l s e r g l u t h r p h e p r o 124

DB 368 g t g a a g g t c t c a c a c a c t g c a c a c g t c a c c t g c c c t g c c t g a g a g a c c t t c c c 427
QY 125 p r o g l y m e t p r o c y s t r p v a l t h r g l y a s p v a l a s p a n a s p g l u a r g l e u p r o 144
DB 428 c c g g a g a t g c c g t g c t g a c t g c g g g c a t t g a c a t t g a g a g c g c t c c a 487
QY 145 p r o p h e p r o l e u l y s g l n v a l l y s v a l p r o l l e m e t g l u s n h i s i l e c y s a s p a l a 164
DB 488 c c g c a t t t c t c t g a a g c a g t g a a g t c c c a t a t t g a a a a c a c a t t t g a g a c g a 547
QY 165 l y s t y r h i s l e u g l y a l a t y r t h r g l y a s p a s p v a l a r g l l e v a l a r a s p a s p m e l e u 184
DB 548 a a a t a c c a c c t t g c g c t g a c a c g g a g a c a g c t c g c a t c g t c g t g a c a g a c a t c t g t 607
QY 185 c y s a l a g l y a n t h r a r g a g a s p s e r c y e g l i n g l y a s p s e r g l y g l y p r o l e u a l c y s 204
DB 608 t g t c c c g g a a c a c c c g a g g a c t c a t g c a g g c a c a t c c g a g g g c c c t g g t g t g c 667
QY 205 l y s v a l a n g l y t h r t r p l e u g l n a l a g l y v a l v a l s e r t r p g l y g l u g l y c y e a l a g l n 224
DB 668 a a g t g a a t g c a c t g c t g c a g c g g c g t g t c a c t g g c a g g c t g t g c c a g 727
QY 225 p r o a n a r p r o g l y l e t y r t h r a r g v a l t h r t y r l e u a s p t r p l i e h i s i e t y r 244
DB 728 c c g a a c c g c c t g g c a t t a c a c c g t g a c c t a c t g a c t t g a c t g a t c a c a c a c t a t 787
QY 245 v a l p r o l y s l y s p r o 249
DB 788 g t c c c a a a a a g c g 802

RESULT 9

US-09-917-254-50
Sequence 50, Application US/09917254

Patent No. 6703204
GENERAL INFORMATION:
APPLICANT: Mutter, George
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/7224 (TRV)
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US/09/917,254
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50
LENGTH: 1081
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-917-254-50

Alignment Scores:

Pred. No.: 4,766-145 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
Gaps: 0

US-09-598-982c-21 (1-249) x US-09-917-254-50 (1-1081)

QY 5 l l e v a l g i y g l i n g l u a l a p r o a r g s e r l y t r p r o t r p g l i n v a l s e r l e u a r g v a l 24
DB 68 a t c g t t g g g g t c a g a g g c c c c a g a g a c a g t g c c t t g c a g a g t g a c t g a g a g t c 127
QY 25 h i s g l y p r o t y r t r p m e t h i s p h e c y s g l y s e r l e u l l e h i s p r o g l i n t r p v a l l e u 44
DB 128 c g c a c c a g t a c t g a t g a c a t t c t g c g g g g c t c c t c a t c a c c c a c a g t g g t g t g t g 187
QY 45 t h r l a a l a a l a c y s v a l g l y p r o a s p v a l l y s a s p l e u a l a l e u a r g v a l g l n l e u 64
DB 188 a c c g a c c a g c a c t g c t g g g a c c g a c g t c a a g a g a t c t g g c c g c c t t c a g g g t g c a a c t g 247

QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
 Db 248 CGGGAGCAGACCTCTACTACACGACCAAGCTCTGCGGTGACGAGTATCATCTGCAC 307
 QY 85 ProGlnPheTyrThrAlaGlnIleGlyValAspIleAlaLeuLeuIleuGluGluPro 104
 Db 308 CCACAGTTCTACACCCCGCAGATCGACCGCATGCGCTGTGAGCTGAGGAGCGCG 367
 QY 105 ValIleValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 368 GTGAAGGTCTCCAGCCACGTCACAGGTCACTCCCTGCCCTCCCTCAGAGACTTCCCC 427
 QY 125 ProGlyMetProCysTyrValThrGlyTyrGlyAspValAspAsnAspGluArgLeuPro 144
 Db 428 CCGGGATGCGCGTGTGCTGCTGCTGCTGCGGCGATGTGACAAATGATGAGCGCTCCCA 487
 QY 145 ProProPheProLeuLeuGlnValIleValValProIleMetGluAsnHisIleCysAspAla 164
 Db 488 CCGCCATTCTCTGAGAGCAGGTGAAGTCCCATTAATGAAAAACCAATTGTGACGCA 547
 QY 165 IysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
 Db 548 AATATACACCTTGCGCGCTTACAGGAGACGATCCGATCGTCCGTACACAGATGCTG 607
 QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 608 TGTGCGGGAGAACCCCGAGGAGCATGCTCAGGCGCATCCGAGGCGCCCTGTGTGTC 667
 QY 205 IysValAsnGlyThrTyrPheGlnAlaGlyValValSerTyrGlyGlnGlyCysAlaGln 224
 Db 668 AAGGTAAATGACCTGCGTGCAGCGCGGTGTGCTGAGGGGCGCAGGGCTGTGCCAG 727
 QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTyrIleHisIstYr 244
 Db 728 CCCAACCGGCTGCGATCTACACCGGTGTACTACTACTTGAACGTGATCCACCACTAT 787
 QY 245 ValProIleValPro 249
 Db 788 GTCCCAAAAAAGCCG 802

RESULT 10
 US-09-016-366A-16
 ; Sequence 16, Application US/09016366A
 ; Patent No. 5955431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chifu
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037, 090
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7093

TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; INDEX:
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1154 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-016-366A-16

Alignment Scores:
 Pred. No.: 6,2e-137 Length: 1154
 Score: 1274.00 Matches: 226
 Percent Similarity: 94.69% Conservative: 6
 Best Local Similarity: 92.24% Mismatches: 13
 Query Match: 91.46% Indels: 0
 DB: 2 Gaps: 0

US-09-598-982C-21 (1-249) x US-09-016-366A-16 (1-1154)

QY 5 IIEValGlyGlnGlnAlaProArgSerLysTyrProTyrPheGlnValSerLeuArgVal 24
 Db 108 ATCTGCGGGGTCAGAGAGCCCGCCAGAGCAAGTGGCCCTGCGAGTGAAGTGC 167
 QY 25 HisGlyProTyrTyrMetHisPheCysGlyGlySerLeuIleHisProGlnTyrValLeu 44
 Db 168 CCGGACCGATCTGATGATGATCTTCTGCGGGGCTCCCTCATTCACCCCAAGGGTGTCTG 227
 QY 45 ThrAlaAlaCysValGlyProAspValIysAspLeuAlaLeuArgValGlnLeu 64
 Db 228 ACCGCGGCGCATGCTGCTGGAGCCGAGCTCAAGATCTGGCCACCTCAGGGTGAACCTG 287
 QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
 Db 288 CGGGAGCAGACCTTACTACACGACGATGCTGCGCCAGTCAGAGATCATCTGTGAC 347
 QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
 Db 348 CCACAGTTCTACATATCATCATGAGAGGATATTCGCCCTGCTGAGACTGGAGAGGCC 407
 QY 105 ValIysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 408 GTGAACATCTCAGCGCGGTCCACACGATCATGCTGCCCTGCTCGGAGACTTCCCC 467
 QY 125 ProGlyMetProCysTyrValThrGlyTyrGlyAspValAspAsnAspGluArgLeuPro 144
 Db 468 CCGGGATGCGCGTGTGCTGCTGCTGCGGCGATGTGACAAATGATGAGCCCTCCCA 527
 QY 145 ProProPheProLeuLeuGlnValIysValProIleMetGluAsnHisIleCysAspAla 164
 Db 528 CCGCATTTCCCTTGAAGCGGTGAAGTCCCATTAATGAAAAACCAATTGTGACGCA 587
 QY 165 IysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
 Db 588 AATATACACCTTGCGCGCTTACAGGAGACGTCGCCATCATCTGAGACGATGCTG 647
 QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 648 TGTGCGGGAGAACAGAGGACCTCTGCAAGGGCGACTGTGAGGGCCCTGTGTGTC 707
 QY 205 IysValAsnGlyThrTyrPheGlnAlaGlyValValSerTyrGlyGlnGlyCysAlaGln 224
 Db 708 AAGGTGAATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 767
 QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTyrIleHisIstYr 244
 Db 768 CCACACCGGCTGCGATCTACACCGGTGTACTACTACTTGAATGATCCACCACTAT 827
 QY 245 ValProIleValPro 249

DB 828 GTCCCAAAAAGCCG 842

RESULT 11

US-08-978-404B-11
Sequence 11, Application US/08978404B
Patent No. 5968782

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:

SEQUENCE CHARACTERISTICS:

LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-978-404B-11

Alignment Scores:

Pred. No.: 6.2e-137 Length: 1154
Score: 1274.00 Matches: 226
Percent Similarity: 94.69% Conservative: 6
Best Local Similarity: 92.24% Mismatches: 13
Query Match: 91.46% Indels: 0
DB: 2 Gaps: 0

US-09-598-982C-21 (1-249) x US-08-978-404B-11 (1-1154)

QY 5 l l e v a l g l y g l i n g l u a l a p r o a r g s e r l y t t p r i o t r p g l i n v a l s e r l e u a r g y a l 24
DB 108 A T C G T C G G G G G T C A G A G A G C C C C C A G A C A A G T G C C C T G C A G A G T G A G C T T C G A G A G T C 167
QY 25 H i s g l y p r o t y r t r m e t h i s p h e c y s g l y g l y s e r l e u l i h i p r o d i n t r p a l l e u 44
DB 168 C C G A C C A T T C A G A T G C A C T T C G C G G G G C C C C T A T C A C C C C A G T G G T G C T G 227
QY 45 T h r a l a a l a c y a v a l g l y p r o a s p v a l l y s a s p l e u a l a l e u a r g y a l g l i n e u 64
DB 228 A C C G G G G C C A C T G C C T G G A C C G A C G T C A A G A T C T G C C A C C C T C A G G G T G C A C T G 287
QY 65 A r g g l u g l i n h i s l e u t y r t y r g l i n a s p g l i n l e u l e u p r o v a l s e r t r g l i l e l e v a l h i s 84
DB 288 C C G A G A C C A C C T T A C T A C C A G A C C A G C T G C T G C C A G T C A G A G A T C A T C G T G C A C 347
QY 85 P r o g l i n p h e t y r t h r a l a g l i n l e g l y a l a s p l i e a l e u l e u g l i n e u g l i n u p r o 104

DB 348 C C A C A G T T T A C A T C A T C A C A C T G A G C G A G A T T C C C C T G C G A G A G C T G A G A G A G C C C 407

QY 105 V a l l y s v a l s e r s e r h i s v a l h i t h r v a l t h r l e u p r o p o a l a s e r g l u t h r p h e p r o 124

DB 408 G T G A A C A T C T C C A C C C G T C C A C A C G G T A C T G C C C C C C T G C C T G C G A G A C C T T C C C C 467

QY 125 P r o g l i m e t p r o c y e t t r p v a l t h r g l y t r p g l y a s p v a l l a s p a n a s p g l u a r g l e u p r o 144

DB 468 C C G A G A G C C G T G C T G G T A C T G C C T G G G C A T G A C A A T G A A G C C C C T C C C A 527

QY 145 P r o p r o p h e p r o l e u l y g l i n v a l l y s v a l p r o l l e m e t g l u a e n h i s l e c y a s p a l a 164

DB 528 C C G C A T T T C C C C G A A G A C G T G A A G T C C C C A T A T G A A A C C A C A T T T G A G A C G A 587

QY 165 L y s t y r h i s l e u g l y a l a t y r t h r g l y a s p a s p v a l l g l e v a l a g a s p a s p m e l e u 184

DB 588 A A A T A C C A C T T G C G C C T A C A C G G A G A C A C C T C C G C A T C A T C C G T G A C G A T G C T G 647

QY 185 C y s a l a g l y a e n t h r a r g a r g a s p s e r c y s g l i n g l y a s p s e r g l y p r o l e u v a l c y s 204

DB 648 T G T C C G G A A C A C C A G A G G A C T C C T G C A A G G C A C T T G A G A G G C C C C T G T G T G C 707

QY 205 L y s v a l s e n g l y t h r t r p l e u g l n a g l y v a l s e r t r p g l y g l u g l y c y a l a g l n 224

DB 708 A A G T G A A T G C A C T G C T A C A G C G G C C T G T C A G T G G A C A G A G G C T G T G C C C A G 767

QY 225 P r o a s n a r p r o g l i l y l e t y r t h r a r g v a l t h r t y r t y r l e u a s p t r p l i h i s t y r 244

DB 768 C C C A A C C G C C T G C A C T T A C A C C G T G C A C T T A C T T G A C T G A T C C A C A C A T A T 827

QY 245 V a l p r o l y s l y s p r o 249

DB 828 G T C C C A A A A A G C C G 842

RESULT 12

US-09-016-366A-14

Sequence 14, Application US/09016366A
Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:

INFORMATION FOR SEQ ID NO: 14:

```
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1108 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-09-016-366A-14

Alignment Scores:
Pred. No.: 7,31e-116 Length: 1108
Score: 1091.00 Matches: 190
Percent Similarity: 86.01% Conservative: 19
Best Local Similarity: 78.19% Mismatches: 34
Query Match: 78.32% Indels: 0
DB: Gaps: 0

US-09-598-982C-21 (1-249) x US-09-016-366A-14 (1-1108)
QY 5 ILeValGlyGlnGlnuAlaProArGSerLySTrPProTrpGlnValSerLeuArGVal 24
Db 127 ATCGTGGAGGACATGAGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCTGAGATT 186
QY 25 HisGlyProTyTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValIleu 44
Db 187 AAATTAACACTGAGTACATTTCTCGGAGGCTCTCTCATCCACACAGTGGGTGCTC 246
QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArGValGlnLeu 64
Db 247 ACTGGCGCACACTGTGTGGACCGGCACATCAAAAGCCACAGCTTCCCGGTGGACGCTT 306
QY 65 ArgGlnGlnHisLeuTyTrpGlnAspGlnLeuProValSerArgIleIleValHis 84
Db 307 CGTGACACAGATATATATATGAGGACCAAGCTCTCTTTGAACCGGATCGGTGTCAC 366
QY 85 ProGlnPheTyTrpAlaGlnIleGlyAlaAspIleAlaLeuGlnLeuGlnuPro 104
Db 367 CCCCACTATTACAGCGCGGAGGTGGGCGACAGCTGCTCTGAGAGCTTGAGTCCCT 426
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGlnuThrPhePro 124
Db 427 GTGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCCCTGCGAGACCTTCCCC 486
QY 125 ProGlnMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db 487 CCGGAGACATCGTGTGGTGGACAGGCTGGGCGACATGATATATACGACGCTTCCCA 546
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGlnuHisIleCysAspAla 164
Db 547 CCTCTTATCTCTGAAGCAAGTGAAGTCCCATTTGTGAAAACAGCCTGTGTACCGG 606
QY 165 LysTyHisLeuGlyAlaTyTrpGlyAspAspValArgIleValArgAspMetLeu 184
Db 607 AAGTACACACCTGGCCCTACACGGGAGATGATTTTCCATTTCCATGATGAGCATGCTG 666
QY 185 CysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 667 TGGCTGGAAATACAGAGAGAGACTCTCTGCAAGGGGAGATTCAAGGGGGCGACGAGTCTG 726
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlnuGlyCysAlaGln 224
Db 727 AAGGTGAGGGTACCTGGCTGCGAGGACGAGGTGTGAGCTGGGGTGAAGGCTTGGACAG 786
QY 225 ProAsnArgProGlyIleTyTrpThrArgValThrTyTrpLeuAspTrpIleHisIleTy 244
Db 787 CCCAACAAGCCTGGCATCTACACCCGGGTGACACTACTTAACTGAGATCCACCGCTAT 846
QY 245 ValProLys 247
Db 847 GTCCTGTAG 855

RESULT 13
US-08-978-404B-20
; Sequence 20, Application US/08978404B
```

```
/ Patent No. 5968782
/ GENERAL INFORMATION:
/ APPLICANT: Stevens, Richard L.
/ TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
/ NUMBER OF INVENTIONS: FIRINDGEN
/ NUMBER OF SEQUENCES: 74
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02210-2211
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/978,404B
/ FILING DATE: 25-NOV-97
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/032,354
/ FILING DATE: 04-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/70930
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1108 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-978-404B-20

Alignment Scores:
Pred. No.: 7,31e-116 Length: 1108
Score: 1091.00 Matches: 190
Percent Similarity: 86.01% Conservative: 19
Best Local Similarity: 78.19% Mismatches: 34
Query Match: 78.32% Indels: 0
DB: Gaps: 0

US-09-598-982C-21 (1-249) x US-08-978-404B-20 (1-1108)
QY 5 ILeValGlyGlnGlnuAlaProArGSerLySTrPProTrpGlnValSerLeuArGVal 24
Db 127 ATCGTGGAGGACATGAGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCTGAGATT 186
QY 25 HisGlyProTyTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValIleu 44
Db 187 AAATTAACACTGAGTACATTTCTCGGAGGCTCTCTCATCCACACAGTGGGTGCTC 246
QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArGValGlnLeu 64
Db 247 ACTGGCGCACACTGTGTGGACCGGCACATCAAAAGCCACAGCTTCCCGGTGGACGCTT 306
QY 65 ArgGlnGlnHisLeuTyTrpGlnAspGlnLeuProValSerArgIleIleValHis 84
Db 307 CGTGACACAGATATATATGAGGACCAAGCTCTCTTTGAACCGGATCGGTGTCAC 366
QY 85 ProGlnPheTyTrpAlaGlnIleGlyAlaAspIleAlaLeuGlnLeuGlnuPro 104
Db 367 CCCCACTATTACAGCGCGGAGGTGGGCGACAGCTGCTCTGAGAGCTTGAGTCCCT 426
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGlnuThrPhePro 124
```



```

ADDRESSER: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-1

Alignment Scores:
Pred. No.: 1,21e-111      Length: 1031
Score: 1054.00           Matches: 186
Percent Similarity: 83.54%      Conservative: 17
Best Local Similarity: 76.54%    Mismatches: 40
Query Match: 75.66%           Indels: 0
DB: 2                      Gaps: 0

US-09-598-982C-21 (1-249) x US-08-978-404B-1 (1-1031)
QY 5 11eva1g1yglnglnua1aProaRgSerLyfTrpTrpGlnvalSerLeuAryVal 24
Db 111 ATTGTGGGGGACAGAGGACATGAGGCAAGTGCGCTCGGAGGTGAGCGCTGCC 170
QY 25 H1sG1yPr0LyTTrpMeth1sPheCySG1yG1ySerLeu11eh1sPr0G1nTTrpVal1eu 44
Db 171 AATGACACCTACTGAGATGATTTCTGCGGTGCTCCCTCATCCACCCACAGTGGGTCTC 230
QY 45 Th1Ala1a1aCySValG1yProaSPVal1ySAspleu1a1a1euaRgValG1n1eu 64
Db 231 ACTGGGGACACGTGTGGGACCGGATGTGCTGACCCCAACAAGTCAGAGTACGCTC 290
QY 65 ArgGluGlnHisLeuTrpTyrGlnAspGlnLeuProValSerArg11e11ValHis 84
Db 291 CGTAAGCAGTACTCTATTACCATGACCAACCTGATGACTGAGCCAGATCATCACACAC 350
QY 85 ProGlnPheTyrThra1aGln11eG1yAlaSer11eAla1euleuGln1euGluPro 104
Db 351 CCCGACTTCTACACTGCTCCAGAGATGGGGACAGACATTCCTGCTGAACTCACAAACCT 410
QY 105 Val1ySValSerSerHisValHisThrVal1ThrLeuProPro1aSerGluThrPhePro 124
Db 411 GTGAACATTTCTGATGATGATCCACCTGTCCTCCCTACCTCCCTCAGAGACCTTCCCC 470
QY 125 ProG1yMeCPProCySTrpVal1ThrG1yTTrpG1yAspVal1AspAsnAspGluArgLeuPro 144
Db 471 TCAGGAACGTTGTGCTGGGTGACAGGCTGGGTGAACATGATGTAAACCTGCCG 530
QY 145 ProProPheProLeu1ySglnVal1ySVal1Pro11eMeTGlusnHis11eCySAspAla 164

```

```

Db 531 CCACATTTCTTTGAAGAGGTGCAAGTCCCATTTATAGAAACACCTTTGTGACTTG 590
QY 165 LysTyrHisLeuG1yAlaTyrThrG1yAspAspValaRg11eVala1aRgAspAspMetLeu 184
Db 591 AAGTATCAAAAGGTCTCATGCACAGTGAACAATGTCACATTTGTCCGAGATGACATGCTG 650
QY 185 CyS1aG1yAsnThrArgAspSerCySG1nG1yAspSerG1yG1yProLeuValCyS 204
Db 651 TGTGCTGGGAATGAAGACATGACTCTGCGAGGCGACTCCGAGAGACCTCTGGTCTGC 710
QY 205 LysVala1aenG1yThrTrpLeuGln1aG1yVal1a1e1SerTrpG1yGluG1yCyS1aGln 224
Db 711 AAGTATGAAGACACCTGCTGAGGCGAGCGGTGACCTGGGGTGAAGGCTGTGCACAG 770
QY 225 ProaMaRgProG1y11eTyrThrArgVal1ThrTyrTyrLeuAspTrp11eh1s1sTyr 244
Db 771 CCCAACAGGCGTGGGATCATGACCCGGGTCACTATTACTTGAGATCGATCCACCATAT 830
QY 245 Val1Pro1yS 247
Db 831 GTCCCAAG 839

```

Search completed: August 27, 2005, 21:26:04
 Job time : 183 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2005, 23:01:40 ; Search time 113 Seconds

(without alignments)
865.829 Million cell updates/sec

Title: US-09-598-982C-21

Perfect score: 1393
Sequence: 1 LEKRVGGQGEAPRSKMPQV.....ITRVITYLDWIMHVPKKP 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1368	98.2	254	14	US-10-131-409-74
2	1368	98.2	254	15	US-10-139-854-74
3	1368	98.2	254	15	US-10-150-813-74
4	1368	98.2	254	15	US-10-150-811-74
5	1368	98.2	256	14	US-10-131-409-92
6	1368	98.2	256	15	US-10-139-854-92
7	1368	98.2	256	15	US-10-150-813-92
8	1368	98.2	256	15	US-10-150-811-92
9	1368	98.2	264	14	US-10-131-409-104
10	1368	98.2	264	15	US-10-139-854-104
11	1368	98.2	264	15	US-10-150-813-104

ALIGNMENTS

12	1368	98.2	264	15	US-10-150-811-104	Sequence 104, App
13	1368	98.2	275	10	US-09-813-432-44	Sequence 48, App1
14	1368	98.2	275	15	US-10-352-684A-48	Sequence 44, App1
15	1368	98.2	275	15	US-10-174-364A-44	Sequence 44, App1
16	1368	98.2	275	15	US-10-246-583-44	Sequence 44, App1
17	1368	98.2	275	15	US-10-287-226-94	Sequence 94, App1
18	1368	98.2	275	15	US-10-689-832-44	Sequence 44, App1
19	1363	97.8	275	15	US-10-287-226-92	Sequence 92, App1
20	1363	97.8	275	16	US-10-723-860-2680	Sequence 2690, App
21	1363	97.8	275	18	US-10-756-149-5451	Sequence 5451, App
22	1347.5	96.7	272	14	US-10-117-323-40	Sequence 40, App1
23	1329	95.4	691	15	US-10-275-505-13	Sequence 13, App1
24	1323	95.0	275	15	US-10-287-226-90	Sequence 90, App1
25	1317	94.5	266	14	US-10-131-409-84	Sequence 84, App1
26	1317	94.5	266	15	US-10-139-854-84	Sequence 84, App1
27	1317	94.5	266	15	US-10-150-813-84	Sequence 84, App1
28	1317	94.5	266	15	US-10-150-811-84	Sequence 84, App1
29	1312	94.2	279	15	US-10-287-226-88	Sequence 88, App1
30	1274	91.5	245	11	US-09-789-210-69	Sequence 69, App1
31	1274	91.5	275	14	US-10-117-323-36	Sequence 36, App1
32	1274	91.5	275	15	US-10-352-684A-46	Sequence 46, App1
33	1270	91.2	231	10	US-09-898-837A-52	Sequence 52, App1
34	1104	79.3	199	14	US-10-131-409-98	Sequence 98, App1
35	1104	79.3	199	15	US-10-139-854-98	Sequence 98, App1
36	1104	79.3	199	15	US-10-150-813-98	Sequence 98, App1
37	1104	79.3	199	15	US-10-150-811-98	Sequence 98, App1
38	1091	78.3	252	10	US-09-813-432-42	Sequence 42, App1
39	1091	78.3	252	15	US-10-174-364-42	Sequence 42, App1
40	1091	78.3	252	15	US-10-246-583-42	Sequence 42, App1
41	1091	78.3	252	16	US-10-689-832-42	Sequence 42, App1
42	1091	78.3	276	14	US-10-117-323-35	Sequence 35, App1
43	1077	77.3	276	14	US-10-111-955-3	Sequence 3, App1
44	1064	76.4	247	14	US-10-131-409-86	Sequence 86, App1
45	1064	76.4	247	15	US-10-139-854-86	Sequence 86, App1

RESULT 1
US-10-131-409-74
; Sequence 74, Application US/10131409
; Publication No. US20030199465A1
; GENERAL INFORMATION:
; APPLICANT: Malyanar et al.
; TITLE OF INVENTION: No. US20030199465A1el Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CIPCOM1
; CURRENT APPLICATION NUMBER: US/10/131,409
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/898,954
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74

LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-409-74

Query Match 98.2%; Score 1368; DB 14; Length 254;
Best Local Similarity 99.6%; Pred. No. 4.2e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKWPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRVQL 64
DB 10 IVGGGEAPRSKWPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRVQL 69
QY 65 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLELEBPVKVSSHVTITLPPASETFP 124
DB 70 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLELEBPVKVSSHVTITLPPASETFP 129
QY 125 PGMPCMVTGMDVNDERLPPPEPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDML 184
DB 130 PGMPCMVTGMDVNDERLPPPEPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDML 189
QY 185 CAGNTRRDSGCGSGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
DB 190 CAGNTRRDSGCGSGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 249
QY 245 VPKKP 249
DB 250 VPKKP 254

RESULT 2
US-10-139-854-74
Sequence 74, Application US/10139854
Publication No. US20030202971A1

GENERAL INFORMATION:

APPLICANT: Majumder, Kumar

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same

FILE REFERENCE: 15966-675CON2

CURRENT APPLICATION NUMBER: US/10/139,854

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 09/783,429

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/182,733

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 60/182,724

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 60/183,896

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 60/184,497

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/224,157

PRIOR FILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: 60/184,482

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/184,744

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/197,083

PRIOR FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: 60/233,405

PRIOR FILING DATE: 2000-09-18

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 126

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 74

LENGTH: 254

TYPE: PRT

ORGANISM: Homo sapiens

US-10-139-854-74

Query Match 98.2%; Score 1368; DB 15; Length 254;
Best Local Similarity 99.6%; Pred. No. 4.2e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKWPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRVQL 64
DB 10 IVGGGEAPRSKWPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRVQL 69
QY 65 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLELEBPVKVSSHVTITLPPASETFP 124
DB 70 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLELEBPVKVSSHVTITLPPASETFP 129
QY 125 PGMPCMVTGMDVNDERLPPPEPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDML 184
DB 130 PGMPCMVTGMDVNDERLPPPEPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDML 189
QY 185 CAGNTRRDSGCGSGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
DB 190 CAGNTRRDSGCGSGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 249
QY 245 VPKKP 249
DB 250 VPKKP 254

RESULT 3
US-10-150-813-74

Sequence 74, Application US/10150813

Publication No. US20030224367A1

GENERAL INFORMATION:

APPLICANT: Majumder

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same

FILE REFERENCE: 15966-675CIPCON2

CURRENT APPLICATION NUMBER: US/10/150,813

CURRENT FILING DATE: 2002-12-03

PRIOR APPLICATION NUMBER: 09/898,954

PRIOR FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: 60/182,733

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 60/182,724

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 60/183,896

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 60/184,497

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/224,157

PRIOR FILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: 60/184,482

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/184,744

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/197,083

PRIOR FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: 60/233,405

PRIOR FILING DATE: 2000-09-18

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 74

LENGTH: 254

TYPE: PRT

ORGANISM: Homo sapiens

US-10-150-813-74

Query Match 98.2%; Score 1368; DB 15; Length 254;
Best Local Similarity 99.6%; Pred. No. 4.2e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKWPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRVQL 64
DB 10 IVGGGEAPRSKWPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRVQL 69
QY 65 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLELEBPVKVSSHVTITLPPASETFP 124
DB 70 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLELEBPVKVSSHVTITLPPASETFP 129
QY 125 PGMPCMVTGMDVNDERLPPPEPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDML 184

```
Db 130 PGMPCWVTGMDVNDERLPPPPFLKQYVPIEMENHICDAKYLGAATGDDVRIVRDML 189
QY 185 CAGNTRRDSGCGDSGGLVCKVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYLLDMIHNY 244
Db 190 CAGNTRRDSGCGDSGGLVCKVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYLLDMIHNY 249
QY 245 VPKKP 249
Db 250 VPKKP 254

RESULT 4
US-10-150-811-74
; Sequence 74, Application US/10150811
; Publication No. US20040010120A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar et al.
; TITLE OF INVENTION: No. US20040010120A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-675CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/150,811
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 09/970,607
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-150-811-74

Query Match 98.2%; Score 1368; DB 15; Length 254;
Best Local Similarity 99.6%; Pred. No. 4,2e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IYGGGEAPRSKMPQVSLRVHGPYWMHFCGSLIHPQVLTAAACVGPVDVLAALRVOL 64
Db 10 IYGGGEAPRSKMPQVSLRVHGPYWMHFCGSLIHPQVLTAAACVGPVDVLAALRVOL 69
QY 65 REOHLTYDQDLPPVSRITVHPQFTTAQIGADIALLELEPVSSSHVHTVTLPPASETFP 124
Db 70 REOHLTYDQDLPPVSRITVHPQFTTAQIGADIALLELEPVSSSHVHTVTLPPASETFP 129
QY 125 PGMPCWVTGMDVNDERLPPPPFLKQYVPIEMENHICDAKYLGAATGDDVRIVRDML 184
Db 130 PGMPCWVTGMDVNDERLPPPPFLKQYVPIEMENHICDAKYLGAATGDDVRIVRDML 189
QY 185 CAGNTRRDSGCGDSGGLVCKVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYLLDMIHNY 244
Db 190 CAGNTRRDSGCGDSGGLVCKVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYLLDMIHNY 249
QY 245 VPKKP 249
Db 250 VPKKP 254
```

```
Db 250 VPKKP 254

RESULT 5
US-10-131-409-92
; Sequence 92, Application US/10131409
; Publication No. US20030199465A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar et al.
; TITLE OF INVENTION: No. US20030199465A1el Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/131,409
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/898,954
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-409-92

Query Match 98.2%; Score 1368; DB 14; Length 256;
Best Local Similarity 99.6%; Pred. No. 4,3e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IYGGGEAPRSKMPQVSLRVHGPYWMHFCGSLIHPQVLTAAACVGPVDVLAALRVOL 64
Db 12 IYGGGEAPRSKMPQVSLRVHGPYWMHFCGSLIHPQVLTAAACVGPVDVLAALRVOL 71
QY 65 REOHLTYDQDLPPVSRITVHPQFTTAQIGADIALLELEPVSSSHVHTVTLPPASETFP 124
Db 72 REOHLTYDQDLPPVSRITVHPQFTTAQIGADIALLELEPVSSSHVHTVTLPPASETFP 131
QY 125 PGMPCWVTGMDVNDERLPPPPFLKQYVPIEMENHICDAKYLGAATGDDVRIVRDML 184
Db 132 PGMPCWVTGMDVNDERLPPPPFLKQYVPIEMENHICDAKYLGAATGDDVRIVRDML 191
QY 185 CAGNTRRDSGCGDSGGLVCKVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYLLDMIHNY 244
Db 192 CAGNTRRDSGCGDSGGLVCKVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYLLDMIHNY 251
QY 245 VPKKP 249
Db 252 VPKKP 256

RESULT 6
US-10-139-854-92
; Sequence 92, Application US/10139854
; Publication No. US20030202971A1
; GENERAL INFORMATION:
; APPLICANT: Majumder, Kumud
```

```
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
/ FILE REFERENCE: 15966-675CON2
/ CURRENT APPLICATION NUMBER: US/10/139,854
/ CURRENT FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: 09/783,429
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: 60/182,733
/ PRIOR FILING DATE: 2000-02-15
/ PRIOR APPLICATION NUMBER: 60/182,724
/ PRIOR FILING DATE: 2000-02-15
/ PRIOR APPLICATION NUMBER: 60/183,896
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: 60/184,497
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/224,157
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/184,482
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,744
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/197,083
/ PRIOR FILING DATE: 2000-04-13
/ PRIOR APPLICATION NUMBER: 60/233,405
/ PRIOR FILING DATE: 2000-09-18
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 126
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 92
/ LENGTH: 256
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-139-854-92

Query Match      98.2%; Score 1368; DB 15; Length 256;
Best Local Similarity 99.6%; Pred. No. 4,3e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKPMQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPVKDLAALRYQL 64
DB 12 IVGGQAPRSKPMQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPVKDLAALRYQL 71
QY 65 REQHLHYDQDLPLVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 124
DB 72 REQHLHYDQDLPLVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 131
QY 125 PGMPCWVTGMDVDNDERLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIYRDDML 184
DB 132 PGMPCWVTGMDVDNDERLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIYRDDML 191
QY 185 CAGNTRRDSQCGDSGGLVCKVNGTWLQAGVSWGCGCAQPNRPGIYTRVYYLDMIHNY 244
DB 192 CAGNTRRDSQCGDSGGLVCKVNGTWLQAGVSWGCGCAQPNRPGIYTRVYYLDMIHNY 251
QY 245 VPKKP 249
DB 252 VPKKP 256

RESULT 7
US-10-150-813-92
/ Sequence 92, Application US/10150813
/ Publication No. US2003024367A1
/ GENERAL INFORMATION:
/ APPLICANT: Malyanekar
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
/ FILE REFERENCE: 15966-675CIP1CON2
/ CURRENT APPLICATION NUMBER: US/10/150,813
/ PRIOR FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: 09/898,954
/ PRIOR FILING DATE: 2001-07-03
/ PRIOR APPLICATION NUMBER: 60/182,733
/ PRIOR FILING DATE: 2000-02-15
/ PRIOR APPLICATION NUMBER: 60/182,724
```

```
/ PRIOR FILING DATE: 2000-02-15
/ PRIOR APPLICATION NUMBER: 60/183,896
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: 60/184,497
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/224,157
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/184,482
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,744
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/197,083
/ PRIOR FILING DATE: 2000-04-13
/ PRIOR APPLICATION NUMBER: 60/233,405
/ PRIOR FILING DATE: 2000-09-18
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 92
/ LENGTH: 256
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-150-813-92

Query Match      98.2%; Score 1368; DB 15; Length 256;
Best Local Similarity 99.6%; Pred. No. 4,3e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKPMQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPVKDLAALRYQL 64
DB 12 IVGGQAPRSKPMQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPVKDLAALRYQL 71
QY 65 REQHLHYDQDLPLVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 124
DB 72 REQHLHYDQDLPLVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 131
QY 125 PGMPCWVTGMDVDNDERLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIYRDDML 184
DB 132 PGMPCWVTGMDVDNDERLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIYRDDML 191
QY 185 CAGNTRRDSQCGDSGGLVCKVNGTWLQAGVSWGCGCAQPNRPGIYTRVYYLDMIHNY 244
DB 192 CAGNTRRDSQCGDSGGLVCKVNGTWLQAGVSWGCGCAQPNRPGIYTRVYYLDMIHNY 251
QY 245 VPKKP 249
DB 252 VPKKP 256

RESULT 8
US-10-150-811-92
/ Sequence 92, Application US/10150811
/ Publication No. US20040010120A1
/ GENERAL INFORMATION:
/ APPLICANT: Malyanekar et al.
/ TITLE OF INVENTION: No. US20040010120A1 Polypeptides and Nucleic Acids Encoding Same
/ FILE REFERENCE: 15966-675CIP2CON1
/ CURRENT APPLICATION NUMBER: US/10/150,811
/ CURRENT FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 09/970,607
/ PRIOR FILING DATE: 2001-10-03
/ PRIOR APPLICATION NUMBER: 60/182,733
/ PRIOR FILING DATE: 2000-02-15
/ PRIOR APPLICATION NUMBER: 60/182,724
/ PRIOR FILING DATE: 2000-02-15
/ PRIOR APPLICATION NUMBER: 60/183,896
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: 60/184,497
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/224,157
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/184,482
```

PRIOR APPLICATION NUMBER: 60/184,744
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/197,083
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/233,405
PRIOR FILING DATE: 2000-09-18
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 92
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-10-150-811-92

Query Match 98.2%; Score 1368; DB 15; Length 256;
Best Local Similarity 99.6%; Pred. No. 4.3e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKMPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRYOL 64
DB 12 IVGGGEAPRSKMPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRYOL 71
QY 65 REQHLYYDOLLPVSRITVHPQFYTAQIGADIALLEBPVKVSSHHTVTLPPASETFP 124
DB 72 REQHLYYDOLLPVSRITVHPQFYTAQIGADIALLEBPVKVSSHHTVTLPPASETFP 131
QY 125 PGMPCWVTGMDVDNDELRPPFPPLKQVKVPIEMNHICDAKYHLGAYTGDDVRIYRDDML 184
DB 132 PGMPCWVTGMDVDNDELRPPFPPLKQVKVPIEMNHICDAKYHLGAYTGDDVRIYRDDML 191
QY 185 CAGNTRDSCCGDSGGLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRVTYLDWIHHY 244
DB 192 CAGNTRDSCCGDSGGLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRVTYLDWIHHY 251
QY 245 VPKKP 249
DB 252 VPKKP 256

RESULT 9
US-10-131-409-104
Sequence 104, Application US/10131409
Publication No. US20030199465A1
GENERAL INFORMATION:
APPLICANT: Malyankar et al.
TITLE OF INVENTION: No. US20030199465A1 Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-675CIPICONT
CURRENT APPLICATION NUMBER: US/10/131,409
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/898,954
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/182,733
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/183,896
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/184,497
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/224,157
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/184,482
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,744
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/197,083
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/233,405
PRIOR FILING DATE: 2000-09-18
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 104
LENGTH: 264
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-409-104

Query Match 98.2%; Score 1368; DB 14; Length 264;
Best Local Similarity 99.6%; Pred. No. 4.4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKMPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRYOL 64
DB 20 IVGGGEAPRSKMPQVSLRVHGPYMMHFCGSSLIHPOVLTAAACVGPDKDLAALRYOL 79
QY 65 REQHLYYDOLLPVSRITVHPQFYTAQIGADIALLEBPVKVSSHHTVTLPPASETFP 124
DB 80 REQHLYYDOLLPVSRITVHPQFYTAQIGADIALLEBPVKVSSHHTVTLPPASETFP 139
QY 125 PGMPCWVTGMDVDNDELRPPFPPLKQVKVPIEMNHICDAKYHLGAYTGDDVRIYRDDML 184
DB 140 PGMPCWVTGMDVDNDELRPPFPPLKQVKVPIEMNHICDAKYHLGAYTGDDVRIYRDDML 199
QY 185 CAGNTRDSCCGDSGGLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRVTYLDWIHHY 244
DB 200 CAGNTRDSCCGDSGGLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRVTYLDWIHHY 259
QY 245 VPKKP 249
DB 260 VPKKP 264

RESULT 10
US-10-139-854-104
Sequence 104, Application US/10139854
Publication No. US20030202971A1
GENERAL INFORMATION:
APPLICANT: Majumder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-675CIPICONT
CURRENT APPLICATION NUMBER: US/10/139,854
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 09/783,429
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,733
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/183,896
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/184,497
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/224,157
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/184,482
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,744
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/197,083
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/233,405
PRIOR FILING DATE: 2000-09-18
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 104
LENGTH: 264
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-854-104

Query Match 98.2%; Score 1368; DB 15; Length 264;
Best Local Similarity 99.6%; Pred. No. 4.4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 5 IVGGQAPRSKMPWQVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPVKDLAALRVOL 64
DB 20 IVGGQAPRSKMPWQVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPVKDLAALRVOL 79
QY 65 REQHLYYQDOLLPVSRITIVHPQFYTAQIGADIALLEBEPVKVSSHVHTVTLPPASSTFP 124
DB 80 REQHLYYQDOLLPVSRITIVHPQFYTAQIGADIALLEBEPVKVSSHVHTVTLPPASSTFP 139
QY 125 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 184
DB 140 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 199
QY 185 CAGNTRRDSGQDSGSGPLVCVKNGTWLOAGVSWGEGCAQPNRPGIYTRVYLLDWIMHHY 244
DB 200 CAGNTRRDSGQDSGSGPLVCVKNGTWLOAGVSWGEGCAQPNRPGIYTRVYLLDWIMHHY 259
QY 245 VPKKP 249
DB 260 VPKKP 264
```

```
RESULT 11
US-10-150-813-104
; Sequence 104, Application US/10150813
; Publication No. US20030224367A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CIP1CON2
; CURRENT APPLICATION NUMBER: US/10/150, 813
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 09/898, 954
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182, 733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182, 724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183, 896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184, 497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224, 157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184, 482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184, 744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197, 083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233, 405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-150-813-104
```

```
Query Match 98.2%; Score 1368; DB 15; Length 264;
Best Local Similarity 99.6%; Pred. No. 4,4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 125 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 184
DB 140 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 199
QY 185 CAGNTRRDSGQDSGSGPLVCVKNGTWLOAGVSWGEGCAQPNRPGIYTRVYLLDWIMHHY 244
DB 200 CAGNTRRDSGQDSGSGPLVCVKNGTWLOAGVSWGEGCAQPNRPGIYTRVYLLDWIMHHY 259
QY 245 VPKKP 249
DB 260 VPKKP 264
```

```
RESULT 12
US-10-150-811-104
; Sequence 104, Application US/10150811
; Publication No. US20040010120A1el Polypeptides and Nucleic Acids Encoding Same
; GENERAL INFORMATION:
; APPLICANT: Malyskar et al.
; TITLE OF INVENTION: No. US20040010120A1el Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/150, 811
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 09/970, 607
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/182, 733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182, 724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183, 896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184, 497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224, 157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184, 482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184, 744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197, 083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233, 405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-150-811-104
```

```
Query Match 98.2%; Score 1368; DB 15; Length 264;
Best Local Similarity 99.6%; Pred. No. 4,4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 IVGGQAPRSKMPWQVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPVKDLAALRVOL 64
DB 20 IVGGQAPRSKMPWQVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPVKDLAALRVOL 79
QY 65 REQHLYYQDOLLPVSRITIVHPQFYTAQIGADIALLEBEPVKVSSHVHTVTLPPASSTFP 124
DB 80 REQHLYYQDOLLPVSRITIVHPQFYTAQIGADIALLEBEPVKVSSHVHTVTLPPASSTFP 139
QY 125 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 184
DB 140 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 199
QY 185 CAGNTRRDSGQDSGSGPLVCVKNGTWLOAGVSWGEGCAQPNRPGIYTRVYLLDWIMHHY 244
DB 200 CAGNTRRDSGQDSGSGPLVCVKNGTWLOAGVSWGEGCAQPNRPGIYTRVYLLDWIMHHY 259
QY 245 VPKKP 249
```

Db 260 VPKP 264

RESULT 13
US-09-813-432-44
; Sequence 44, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamid
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Verneet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1 Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-432-44

Query Match 98.2%; Score 1368; DB 10; Length 275;
Best Local Similarity 99.6%; Pred. No. 4.7e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKMPQVSLRVHGPYWMHFCGSLIHPQVLTAAACVGPVDKDLAALRVOL 64
DB 31 IVGGGEAPRSKMPQVSLRVHGPYWMHFCGSLIHPQVLTAAACVGPVDKDLAALRVOL 90
QY 65 REQHLYYODQLLPVSRITVHPQFTTAQIGADIALLEBPVKVSSHVTTLPPASETFP 124
DB 91 REQHLYYODQLLPVSRITVHPQFTTAQIGADIALLEBPVKVSSHVTTLPPASETFP 150
QY 125 PGMPCWVTGMDVNDERLPPRPPLKQVVPIMENHICDAKYHLAGYTGDDVRIVRDDML 184
DB 151 PGMPCWVTGMDVNDERLPPRPPLKQVVPIMENHICDAKYHLAGYTGDDVRIVRDDML 210
QY 185 CAGNTRRDSGCGDSGGPLVCVNGTWTLAGVVSWEBCAQPNRPGIYTRVITYLDWIHHY 244
DB 211 CAGNTRRDSGCGDSGGPLVCVNGTWTLAGVVSWEBCAQPNRPGIYTRVITYLDWIHHY 270
QY 245 VPKP 249
DB 271 VPKP 275

RESULT 14
US-10-352-684A-48

; Sequence 48, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MP102-019P1RMONIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-352-684A-48

Query Match 98.2%; Score 1368; DB 15; Length 275;
Best Local Similarity 99.6%; Pred. No. 4.7e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKMPQVSLRVHGPYWMHFCGSLIHPQVLTAAACVGPVDKDLAALRVOL 64
DB 31 IVGGGEAPRSKMPQVSLRVHGPYWMHFCGSLIHPQVLTAAACVGPVDKDLAALRVOL 90
QY 65 REQHLYYODQLLPVSRITVHPQFTTAQIGADIALLEBPVKVSSHVTTLPPASETFP 124
DB 91 REQHLYYODQLLPVSRITVHPQFTTAQIGADIALLEBPVKVSSHVTTLPPASETFP 150
QY 125 PGMPCWVTGMDVNDERLPPRPPLKQVVPIMENHICDAKYHLAGYTGDDVRIVRDDML 184
DB 151 PGMPCWVTGMDVNDERLPPRPPLKQVVPIMENHICDAKYHLAGYTGDDVRIVRDDML 210
QY 185 CAGNTRRDSGCGDSGGPLVCVNGTWTLAGVVSWEBCAQPNRPGIYTRVITYLDWIHHY 244
DB 211 CAGNTRRDSGCGDSGGPLVCVNGTWTLAGVVSWEBCAQPNRPGIYTRVITYLDWIHHY 270
QY 245 VPKP 249
DB 271 VPKP 275

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2005, 21:22:59 ; Search time 62 Seconds
(without alignments)
299.800 Million cell updates/sec

Title: US-09-598-982C-21

Perfect score: 1393

Sequence: 1 LEKRIVGQGEAPRSKMPQV.....ITYRTVYLDWIMHVPKPP 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	99.6	249	3	US-09-079-970A-5
2	1368	98.2	245	3	US-09-079-970A-6
3	1368	98.2	245	4	US-09-601-318-1
4	1368	98.2	274	2	US-09-016-366A-21
5	1368	98.2	274	2	US-08-978-404B-16
6	1363	97.8	273	2	US-09-016-366A-19
7	1363	97.8	273	2	US-08-978-404B-14
8	1361	97.7	244	4	US-09-601-318-4
9	1361	97.7	244	4	US-09-601-318-5
10	1361	97.7	244	4	US-09-601-318-6
11	1361	97.7	244	4	US-09-601-318-7
12	1344	96.5	267	2	US-09-016-366A-23
13	1344	96.5	267	2	US-08-978-404B-18
14	1344	96.5	267	4	US-09-917-254-101
15	1274	91.5	245	3	US-08-944-483-69
16	1274	91.5	275	2	US-09-016-366A-17
17	1274	91.5	275	2	US-08-978-404B-12
18	1091	78.3	276	2	US-09-016-366A-15
19	1091	78.3	276	2	US-08-978-404B-21
20	1075	77.2	270	2	US-08-978-404B-8
21	1054	75.7	273	2	US-08-978-404B-3
22	1051	75.4	274	2	US-08-978-404B-5
23	1037	74.4	273	2	US-08-978-404B-6
24	702	50.4	190	3	US-08-845-998-4
25	702	50.4	190	3	US-09-206-537-4
26	702	50.4	190	3	US-09-430-854-4
27	698	50.1	190	2	US-08-845-998-6

28	698	50.1	190	3	US-09-206-537-6	Sequence 6, Appli
29	698	50.1	190	3	US-09-430-854-6	Sequence 6, Appli
30	684.5	49.1	269	2	US-08-978-404B-10	Sequence 10, Appli
31	563.5	40.5	290	4	US-09-386-653A-7	Sequence 7, Appli
32	554.5	39.8	315	4	US-09-386-653A-9	Sequence 9, Appli
33	536.5	38.5	284	4	US-09-387-375-7	Sequence 7, Appli
34	536.5	38.5	284	4	US-10-041-400A-7	Sequence 7, Appli
35	536.5	38.5	284	4	US-10-042-091A-7	Sequence 7, Appli
36	527.5	37.9	316	4	US-09-387-375-9	Sequence 9, Appli
37	527.5	37.9	316	4	US-10-041-400A-9	Sequence 9, Appli
38	527.5	37.9	316	4	US-10-042-091A-9	Sequence 9, Appli
39	507	36.4	319	4	US-09-386-642-12	Sequence 12, Appli
40	507	36.4	328	4	US-09-386-642-11	Sequence 11, Appli
41	506	36.3	299	3	US-08-944-483-66	Sequence 6, Appli
42	501.5	36.0	317	4	US-09-386-629-7	Sequence 7, Appli
43	501.5	36.0	317	4	US-09-907-794A-263	Sequence 263, App
44	501.5	36.0	317	4	US-09-905-125A-263	Sequence 263, App
45	501.5	36.0	317	4	US-09-902-775A-263	Sequence 263, App

ALIGNMENTS

RESULT 1
US-09-079-970A-5
Sequence 5, Application US/09079970A
Patent No. 6274366
GENERAL INFORMATION:
APPLICANT: Mafilt, Mark A.
APPLICANT: Niles, Andrew L.
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Trypsin and Method of Making Same
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Intellectual Property Department
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34506.073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-079-970A-5

Query Match 99.6%; Score 1387; DB 3; Length 249;
Best Local Similarity 99.6%; Pred. No. 7.8e-141;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEKRIVGQGEAPRSKMPQVSLRVHGPYWMHFCGSLHPQWVLTAAACVCPDYKDLAAL 60
DB 1 LEKRIVGQGEAPRSKMPQVSLRVHGPYWMHFCGSLHPQWVLTAAACVCPDYKDLAAL 60

QY 61 RVQLREOHLYYOQQLPVSRILIVHPQFYTAQIGADIALLEBEPVYVSSHVHTVTLPPAS 120
|
|
|
Db 61 RVQLREOHLYYOQQLPVSRILIVHPQFYTAQIGADIALLEBEPVYVSSHVHTVTLPPAS 120
|
|
|
QY 121 ETTPPGKPCWVTGMDVNDERLPPPEPLKQVVPIMENHICDAKYHLGAYTGDDVRIYR 180
|
|
|
Db 121 ETTPPGKPCWVTGMDVNDERLPPPEPLKQVVPIMENHICDAKYHLGAYTGDDVRIYR 180
|
|
|
QY 181 DDMLCAGNTRRDSGQDSGGLVCKVNGTWMQAGVSWGEGCAQPNRPGLYTRVYYLDM 240
|
|
|
Db 181 DDMLCAGNTRRDSGQDSGGLVCKVNGTWMQAGVSWGEGCAQPNRPGLYTRVYYLDM 240
|
|
|
QY 241 IHHYVPKKP 249
|
|
|
Db 241 IHHYVPKKP 249
|
|
|

RESULT 2

US-09-079-970A-6
; Sequence 6, Application US/09079970A
; Patent No. 6274366
; GENERAL INFORMATION:
; APPLICANT: Maffitt, Mark A.
; APPLICANT: Niles, Andrew L.
; APPLICANT: Haak-Frendsch, Mary
; TITLE OF INVENTION: Biologically-Active Recombinant Human
; TITLE OF INVENTION: Beta-Trypsin and Method of Making Same
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property Department
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,970A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506.073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-079-970A-6

Query Match 98.2%; Score 1368; DB 3; Length 245;
Best Local Similarity 99.6%; Pred. No. 8.4e-139;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQEARPSKWPQVSLRVHGPYWMHFCGSSLIHPOWVLTAAACVGPVDKDLAALRYOL 64
|
|
|
Db 1 IVGGQEARPSKWPQVSLRVHGPYWMHFCGSSLIHPOWVLTAAACVGPVDKDLAALRYOL 60
|
|
|
QY 65 REOHLYYOQQLPVSRILIVHPQFYTAQIGADIALLEBEPVYVSSHVHTVTLPPASETP 124
|
|
|
Db 61 REOHLYYOQQLPVSRILIVHPQFYTAQIGADIALLEBEPVYVSSHVHTVTLPPASETP 120
|
|
|
QY 125 PGMPCWVTGMDVNDERLPPPEPLKQVVPIMENHICDAKYHLGAYTGDDVRIYRDM 184
|
|
|

Db 121 PGMPCWVTGMDVNDERLPPPEPLKQVVPIMENHICDAKYHLGAYTGDDVRIYRDM 180
|
|
|
QY 185 CAGNTRRDSGQDSGGLVCKVNGTWMQAGVSWGEGCAQPNRPGLYTRVYYLDMIH 244
|
|
|
Db 181 CAGNTRRDSGQDSGGLVCKVNGTWMQAGVSWGEGCAQPNRPGLYTRVYYLDMIH 240
|
|
|
QY 245 VPKKP 249
|
|
|
Db 241 VPKKP 245
|
|
|

RESULT 3

US-09-601-318-1
; Sequence 1, Application US/09601318
; Patent No. 6613769
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Gesellschaft z. Fnd. d. Wissensch. e.V
; APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
; APPLICANT: Bode, Wolfram
; APPLICANT: Moroder, Luis
; APPLICANT: Pereira, Pedro Jose Barbosa
; APPLICANT: Berger, Andreas
; APPLICANT: Huber, Robert
; APPLICANT: Sommerhoff, Christian
; APPLICANT: Schaschke, No. 6613769bert
; APPLICANT: Br, Thomas
; APPLICANT: Martin, Thomas
; APPLICANT: Stadlwieser, Josef
; APPLICANT: Ulrich, Wolf-Rdiger
; APPLICANT: Dominik, Andreas
; APPLICANT: Thibaut, Ulrich
; APPLICANT: Bundschuh, Daniela
; APPLICANT: Beume, Rolf
; APPLICANT: Goebel, Karl-Josef
; TITLE OF INVENTION: Trypsin-Inhibitors
; FILE REFERENCE: 17674P WO-1
; CURRENT APPLICATION NUMBER: US/09/601,318
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: DE19804761.4
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: DE19851300.3
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-601-318-1

Query Match 98.2%; Score 1368; DB 4; Length 245;
Best Local Similarity 99.6%; Pred. No. 8.4e-139;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQEARPSKWPQVSLRVHGPYWMHFCGSSLIHPOWVLTAAACVGPVDKDLAALRYOL 64
|
|
|
Db 1 IVGGQEARPSKWPQVSLRVHGPYWMHFCGSSLIHPOWVLTAAACVGPVDKDLAALRYOL 60
|
|
|
QY 65 REOHLYYOQQLPVSRILIVHPQFYTAQIGADIALLEBEPVYVSSHVHTVTLPPASETP 124
|
|
|
Db 61 REOHLYYOQQLPVSRILIVHPQFYTAQIGADIALLEBEPVYVSSHVHTVTLPPASETP 120
|
|
|
QY 125 PGMPCWVTGMDVNDERLPPPEPLKQVVPIMENHICDAKYHLGAYTGDDVRIYRDM 184
|
|
|
Db 121 PGMPCWVTGMDVNDERLPPPEPLKQVVPIMENHICDAKYHLGAYTGDDVRIYRDM 180
|
|
|
QY 185 CAGNTRRDSGQDSGGLVCKVNGTWMQAGVSWGEGCAQPNRPGLYTRVYYLDMIH 244
|
|
|
Db 181 CAGNTRRDSGQDSGGLVCKVNGTWMQAGVSWGEGCAQPNRPGLYTRVYYLDMIH 240
|
|
|
QY 245 VPKKP 249
|
|
|
Db 241 VPKKP 245
|
|
|


```
/ GENERAL INFORMATION:
/ APPLICANT: Stevens, Richard L.
/ APPLICANT: Huang, Chifu
/ TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
/ TITLE OF INVENTION: INHIBITORS
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02210-2211
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,366A
/ FILING DATE: January 30, 1998
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/037,090
/ FILING DATE: 05-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/7093
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 273 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-016-366A-19

Query Match          97.8%; Score 1363; DB 2; Length 273;
Best Local Similarity 99.2%; Pred. No.3.4e-138;
Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKMPQWVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPVVDLALRVQL 64
DB 29 IVGGGEAPRSKMPQWVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPVVDLALRVQL 88
QY 65 REQHLYYQDQLPVSRIIVHPOFYTAQIGADIALLELEBPVYKSSHHTVTLPPASETFP 124
DB 89 REQHLYYQDQLPVSRIIVHPOFYTAQIGADIALLELEBPVYKSSHHTVTLPPASETFP 148
QY 125 PGMPCMVTGMDGVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIYRDDML 184
DB 149 PGMPCMVTGMDGVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIYRDDML 208
QY 185 CAGNTRRDSGCGDSGSLVCKVNGTWLQAGVWSWGCGAQNRRPGIYTRVYIYLDWIHHY 244
DB 209 CAGNTRRDSGCGDSGSLVCKVNGTWLQAGVWSWGCGAQNRRPGIYTRVYIYLDWIHHY 268
QY 245 VPKKP 249
DB 269 VPKKP 273

RESULT 7
US-08-978-404B-14
/ Sequence 14, Application US/08978404B
/ Patent No. 5968782
/ GENERAL INFORMATION:
/ APPLICANT: Stevens, Richard L.
/ TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
```

```
/ TITLE OF INVENTION: FIBRINOGEN
/ NUMBER OF SEQUENCES: 74
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02210-2211
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/978,404B
/ FILING DATE: 25-NOV-97
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/032,354
/ FILING DATE: 04-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/7090
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 273 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 5968782e
/
US-08-978-404B-14

Query Match          97.8%; Score 1363; DB 2; Length 273;
Best Local Similarity 99.2%; Pred. No.3.4e-138;
Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKMPQWVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPVVDLALRVQL 64
DB 29 IVGGGEAPRSKMPQWVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPVVDLALRVQL 88
QY 65 REQHLYYQDQLPVSRIIVHPOFYTAQIGADIALLELEBPVYKSSHHTVTLPPASETFP 124
DB 89 REQHLYYQDQLPVSRIIVHPOFYTAQIGADIALLELEBPVYKSSHHTVTLPPASETFP 148
QY 125 PGMPCMVTGMDGVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIYRDDML 184
DB 149 PGMPCMVTGMDGVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIYRDDML 208
QY 185 CAGNTRRDSGCGDSGSLVCKVNGTWLQAGVWSWGCGAQNRRPGIYTRVYIYLDWIHHY 244
DB 209 CAGNTRRDSGCGDSGSLVCKVNGTWLQAGVWSWGCGAQNRRPGIYTRVYIYLDWIHHY 268
QY 245 VPKKP 249
DB 269 VPKKP 273

RESULT 8
US-09-601-318-4
/ Sequence 4, Application US/09601318
/ Patent No. 6613769
/ GENERAL INFORMATION:
/ APPLICANT: Max-Planck-Gesellschaft z. Fkd. d. Wissensch. e.V
/ APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
/ APPLICANT: Bode, Wolfram
/ APPLICANT: Moroder, Luis
/ APPLICANT: Pereira, Pedro Jose Barbosa
```

APPLICANT: Bergner, Andreas
APPLICANT: Huber, Robert
APPLICANT: Sommerhoff, Christian
APPLICANT: Schaschke, No. 6613769bert
APPLICANT: Br, Thomas
APPLICANT: Martin, Thomas
APPLICANT: Stadlwieser, Josef
APPLICANT: Ulrich, Wolf-Rdiger
APPLICANT: Dominik, Andreas
APPLICANT: Thibaut, Ulrich
APPLICANT: Bundschuh, Daniela
APPLICANT: Beume, Rolf
APPLICANT: Goebel, Karl-Josef
TITLE OF INVENTION: Typtase-Inhibitoren
FILE REFERENCE: 17674P WO-1
CURRENT APPLICATION NUMBER: US/09/601.318
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: DE19804761.4
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: DE19851300.3
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-601-318-4

Query Match 97.7%; Score 1361; DB 4; Length 244;
Best Local Similarity 99.6%; Pred. No. 4.7e-138;
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKMPQVSLRVHGPYMHFCCGSLIHPOWVLTAAACVGPVDVLDLALRVQL 64
DB 1 IVGGGEAPRSKMPQVSLRVHGPYMHFCCGSLIHPOWVLTAAACVGPVDVLDLALRVQL 60
QY 65 REQHLYYQDOLLPSRIIVHPQFYTAQIGADIALLEBPVKSSSHVHTVTLPPASETFP 124
DB 61 REQHLYYQDOLLPSRIIVHPQFYTAQIGADIALLEBPVKSSSHVHTVTLPPASETFP 120
QY 125 PGMPCTWTGMDVNDRLPPFPPLKQVPIIMENHI CDAKYHLGAYTGDDVRIVRDML 184
DB 121 PGMPCTWTGMDVNDRLPPFPPLKQVPIIMENHI CDAKYHLGAYTGDDVRIVRDML 180
QY 185 CAGNTRRDSGCGSGPLVCVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYYLDMIHXY 244
DB 181 CAGNTRRDSGCGSGPLVCVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYYLDMIHXY 240
QY 245 VPKK 248
DB 241 VPKK 244

RESULT 9
US-09-601-318-5

/ Sequence 5, Application US/09601318
/ Patent No. 6613769
/ GENERAL INFORMATION:
/ APPLICANT: Max-Planck-Gesellschaft z. Frd. d. Wissenssch. e.V
/ APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
/ APPLICANT: Bode, Wolfram
/ APPLICANT: Moroder, Luis
/ APPLICANT: Pereira, Pedro Jose Barbosa
/ APPLICANT: Bergner, Andreas
/ APPLICANT: Huber, Robert
/ APPLICANT: Stadlwieser, Josef
/ APPLICANT: Schaschke, No. 6613769bert
/ APPLICANT: Br, Thomas
/ APPLICANT: Martin, Thomas
/ APPLICANT: Stadlwieser, Josef
/ APPLICANT: Ulrich, Wolf-Rdiger
/ APPLICANT: Dominik, Andreas

APPLICANT: Thibaut, Ulrich
APPLICANT: Bundschuh, Daniela
APPLICANT: Beume, Rolf
APPLICANT: Goebel, Karl-Josef
TITLE OF INVENTION: Typtase-Inhibitoren
FILE REFERENCE: 17674P WO-1
CURRENT APPLICATION NUMBER: US/09/601.318
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: DE19804761.4
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: DE19851300.3
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-601-318-5

Query Match 97.7%; Score 1361; DB 4; Length 244;
Best Local Similarity 99.6%; Pred. No. 4.7e-138;
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGGEAPRSKMPQVSLRVHGPYMHFCCGSLIHPOWVLTAAACVGPVDVLDLALRVQL 64
DB 1 IVGGGEAPRSKMPQVSLRVHGPYMHFCCGSLIHPOWVLTAAACVGPVDVLDLALRVQL 60
QY 65 REQHLYYQDOLLPSRIIVHPQFYTAQIGADIALLEBPVKSSSHVHTVTLPPASETFP 124
DB 61 REQHLYYQDOLLPSRIIVHPQFYTAQIGADIALLEBPVKSSSHVHTVTLPPASETFP 120
QY 125 PGMPCTWTGMDVNDRLPPFPPLKQVPIIMENHI CDAKYHLGAYTGDDVRIVRDML 184
DB 121 PGMPCTWTGMDVNDRLPPFPPLKQVPIIMENHI CDAKYHLGAYTGDDVRIVRDML 180
QY 185 CAGNTRRDSGCGSGPLVCVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYYLDMIHXY 244
DB 181 CAGNTRRDSGCGSGPLVCVNGTWTLOAGVSWGEGCAQPNRPGIYTRVYYLDMIHXY 240
QY 245 VPKK 248
DB 241 VPKK 244

RESULT 10
US-09-601-318-6

/ Sequence 6, Application US/09601318
/ Patent No. 6613769
/ GENERAL INFORMATION:
/ APPLICANT: Max-Planck-Gesellschaft z. Frd. d. Wissenssch. e.V
/ APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
/ APPLICANT: Bode, Wolfram
/ APPLICANT: Moroder, Luis
/ APPLICANT: Pereira, Pedro Jose Barbosa
/ APPLICANT: Bergner, Andreas
/ APPLICANT: Huber, Robert
/ APPLICANT: Stadlwieser, Josef
/ APPLICANT: Schaschke, No. 6613769bert
/ APPLICANT: Br, Thomas
/ APPLICANT: Martin, Thomas
/ APPLICANT: Stadlwieser, Josef
/ APPLICANT: Ulrich, Wolf-Rdiger
/ APPLICANT: Bundschuh, Daniela
/ APPLICANT: Beume, Rolf
/ APPLICANT: Goebel, Karl-Josef
TITLE OF INVENTION: Typtase-Inhibitoren
FILE REFERENCE: 17674P WO-1
CURRENT APPLICATION NUMBER: US/09/601.318
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: DE19804761.4

```
/ PRIOR FILING DATE: 1998-02-06
/ PRIOR APPLICATION NUMBER: DE19851300.3
/ PRIOR FILING DATE: 1998-11-06
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 244
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-601-318-6

Query Match          97.7%; Score 1361; DB 4; Length 244;
Best Local Similarity 99.6%; Pred. No. 4.7e-138;
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDKDLAALRYQL 64
DB 1 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDKDLAALRYQL 60
QY 65 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLEBPVKVSSHHTVTLPPASETFP 124
DB 61 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLEBPVKVSSHHTVTLPPASETFP 120
QY 125 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDDML 184
DB 121 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDDML 180
QY 185 CAGNTRRDSGCGDSGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
DB 181 CAGNTRRDSGCGDSGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 240
QY 245 VPCK 248
DB 241 VPCK 244

RESULT 11
US-09-601-318-7
/ Sequence 7, Application US/09601318
/ Patent No. 6613769
/ GENERAL INFORMATION:
/ APPLICANT: Max-Planck-Gesellschaft z. Fnd. d. Wissensch. e.V
/ APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
/ APPLICANT: Bode, Wolfram
/ APPLICANT: Moroder, Luis
/ APPLICANT: Pereira, Pedro Jose Barbosa
/ APPLICANT: Bergner, Andreas
/ APPLICANT: Huber, Robert
/ APPLICANT: Sommerhoff, Christian
/ APPLICANT: Schaschke, No. 6613769bert
/ APPLICANT: Br, Thomas
/ APPLICANT: Martin, Thomas
/ APPLICANT: Stadlrieser, Josef
/ APPLICANT: Ulrich, Wolf-Rdiger
/ APPLICANT: Dominik, Andreas
/ APPLICANT: Thibaut, Ulrich
/ APPLICANT: Bundeschuh, Daniela
/ APPLICANT: Beume, Rolf
/ APPLICANT: Goedel, Karl-Josef
/ TITLE OF INVENTION: Trypsase-Inhibitoren
/ FILE REFERENCE: 17674P WO-1
/ CURRENT APPLICATION NUMBER: US/09/601,318
/ PRIOR FILING DATE: 2001-01-22
/ PRIOR APPLICATION NUMBER: DE19804761.4
/ PRIOR FILING DATE: 1998-02-06
/ PRIOR APPLICATION NUMBER: DE19851300.3
/ PRIOR FILING DATE: 1998-11-06
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 244
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```

```
US-09-601-318-7

Query Match          97.7%; Score 1361; DB 4; Length 244;
Best Local Similarity 99.6%; Pred. No. 4.7e-138;
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDKDLAALRYQL 64
DB 1 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDKDLAALRYQL 60
QY 65 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLEBPVKVSSHHTVTLPPASETFP 124
DB 61 REQHLYYODQLPVSRIIVHPQFYTAQIGADIALLEBPVKVSSHHTVTLPPASETFP 120
QY 125 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDDML 184
DB 121 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDDML 180
QY 185 CAGNTRRDSGCGDSGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
DB 181 CAGNTRRDSGCGDSGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 240
QY 245 VPCK 248
DB 241 VPCK 244
```

```
RESULT 12
US-09-016-366A-23
/ Sequence 23, Application US/09016366A
/ Patent No. 5955431
/ GENERAL INFORMATION:
/ APPLICANT: Stevens, Richard L.
/ APPLICANT: Huang, Chifu
/ TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02210-2211
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,366A
/ FILING DATE: January 30, 1998
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/037,090
/ FILING DATE: 05-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/7093
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-016-366A-23

Query Match          96.5%; Score 1344; DB 2; Length 267;
```

[illegible]

```

RESULT 14
US-09-917-254-101
; Sequence 101, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Muter, George
; APPLICANT: Baak, Jan
; TITLE OR INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 267
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-09-917-254-101

Query Match      96.5%; Score 1344; DB 4; Length 267;
Best Local Similarity 98.4%; Pred. No. 3.6e-136;
Matches 241; Conservative 0; Mismatches 4; Indels 0; Gaps 0,

QY      5  IVGGQEARPRSKFMPQVSLRHYGHPYWMHFCGGSLLHPQWVLTAAACVGPDVXDIALARVOL 64
DB      23  IVGGQEARPRSKFMPQVSLRHYGHPYWMHFCGGSLLHPQWVLTAAACVGPDVXDIALARVOL 82

QY      65  REQHLIYQDQLLPVSRITIVHPQFTAOIGADIALLEBEPKVSNNITVTLPPASSTFP 124
DB      83  REQHLIYQDQLLPVSRITIVHPQFTAOIGADIALLEBEPKVSNNITVTLPPASSTFP 142

QY      125  PGMFCWVTGMDVNDRLPPPEPLKQVKVIMENH1CDACYH1GAYTGDDVRIYRDML 184
DB      143  PGMFCWVTGMDVNDRLPPPEPLKQVKVIMENH1CDACYH1GAYTGDDVRIYRDML 202

QY      185  CAGNTRRDS CGSDSGGFLVCVKNSTWLDAGVSVSGEGCAQPNRPGIYTRVYYLDMIHYY 244
DB      203  CAGNTRRDS CGSDSGGFLVCVKNSTWLDAGVSVSGEGCAQPNRPGIYTRVYYLDMIHYY 262

QY      245  VPKKP 249
DB      263  VPKKP 267

RESULT 15
US-08-944-483-69
; Sequence 69, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE

```

Job time : 64 secs

APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-69

Query Match 91.5%; Score 1274; DB 3; Length 245;
Best Local Similarity 92.2%; Pred. No. 1.1e-128;
Matches 226; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
QY 5 IVGGQAPRSKMPWQVSLRVHGGPYMMHFCGSLIHPQWLTAAACVDPDKDLAALRVOL 64
DB 1 IVGGQAPRSKMPWQVSLRVDRYMMHFCGSLIHPQWLTAAACGPDVKDLATLRVOL 60
QY 65 REQHLTYQDQLPVSRILVHPQFYTAQIGADIALLELEBPVKYSSHHTVTLLPPASETPP 124
DB 61 REQHLTYQDQLPVSRILVHPQFYIIQTGADIALLELEBPVNISRVHTVMLPPASETPP 120
QY 125 PGMPICAVTGMGDVNDERLPPPEPLKQKVPIIMENHICDAKYHLGAYTGDVDRIVRDDML 184
DB 121 PGMPICAVTGMGDVNDERLPPPEPLKQKVPIIMENHICDAKYHLGAYTGDVDRILRDDML 180
QY 185 CAGNTRRDSGQDGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDWIHHY 244
DB 181 CAGNSGRDSCGDSGGLVCKVNGTWLQAGVSWDEGCAQPNRPGIYTRVYYLDWIHHY 240
QY 245 VPKKP 249
DB 241 VPKKP 245

Search completed: August 27, 2005, 23:13:02

Sequence 2126, Ap

PRIOR FILING DATE: 2002-06-2

?
 ? PRIOR APPLICATION NUMBER: US 60/386,494
 ?
 ? PRIOR FILING DATE: 2002-06-06
 ?
 ? PRIOR APPLICATION NUMBER: US 60/390,965
 ?
 ? PRIOR FILING DATE: 2002-06-24
 ?

```
/ PRIOR APPLICATION NUMBER: US 60/392,480
/ PRIOR FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: US 60/394,128
/ PRIOR FILING DATE: 2002-07-03
/ PRIOR APPLICATION NUMBER: US 60/399,783
/ PRIOR FILING DATE: 2002-07-31
/ PRIOR APPLICATION NUMBER: US 63/403,221
/ PRIOR FILING DATE: 2002-08-13
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 47
/ LENGTH: 1143
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (6)...(833)
US-10-352-684A-47
```

Query Match 94.8%; Score 731; DB 17; Length 1143;

Best Local Similarity 98.0%; Pred. No. 2 6e-195; Mismatches 15; Indels 0; Gaps 0;

Matches 740; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
QY 17 GAATCGTCGGGGGTCAAGAGGCCCCCAAGAGCAAGTGGCCCTGSCAGGTGAGCCTGAGAG 76
DB 94 GCATCGTGGGGGTCAAGAGGCCCCCAAGAGCAAGTGGCCCTGSCAGGTGAGCCTGAGAG 153
QY 77 TCCACGGGCCATCTGATGATCTTCTGCGGGGGCTCCCTCATCCACCCCACTGGGTGC 136
DB 154 TCCACGGGCCATCTGATGATCTTCTGCGGGGGCTCCCTCATCCACCCCACTGGGTGC 213
QY 137 TGACCGCGCGGGGTGGGAGCGGACGTCGAAGATCTGGCGCCCTCAGGGTCAAC 196
DB 214 TGACCGGAGGCACTGGTGGGACCGGACGTCGAAGATCTGGCGCCCTCAGGGTCAAC 273
QY 197 TGGGGAGGAGCACTCTACTACAGGACCAAGTGTCTGGGTGAGCAATGATGAGCGCTCC 256
DB 274 TGGGGAGGAGCACTCTACTACAGGACCAAGTGTCTGGGTGAGCAATGATGAGCGCTCC 333
QY 257 ACCCAGGTTCTACCGCCCAATGGAGGAGCAATCGCCCTGCTGGAGCTGGAGAGAC 316
DB 334 ACCCAGGTTCTACCGCCCAATGGAGGAGCAATCGCCCTGCTGGAGCTGGAGAGAC 393
QY 317 CGGTGAAGTCTCTCAGGCACTGTCACAGGTCACCGTCCCTGCTGAGAGACCTTCC 376
DB 394 CGGTGAAGTCTCTCAGGCACTGTCACAGGTCACCGTCCCTGCTGAGAGACCTTCC 453
QY 377 CCGCGGGAGTGGCTGTGGGTCACTGGCTGGGGCAATGTGACCAATGATGAGCGCTCC 436
DB 454 CCGCGGGAGTGGCTGTGGGTCACTGGCTGGGGCAATGTGACCAATGATGAGCGCTCC 513
QY 437 CACCGCATTTCTCTGAGACAGGTGAAGTCCCAATGAAGAAACCAATTGTGAGG 496
DB 514 CACCGCATTTCTCTGAGACAGGTGAAGTCCCAATGAAGAAACCAATTGTGAGG 573
QY 497 CAAATATCACTTGGGCTTAACAGGAGACAGACGTCGATCGTCCGTGACGATGC 556
DB 574 CAAATATCACTTGGGCTTAACAGGAGACAGACGTCGATCGTCCGTGACGATGC 633
QY 557 TGTGTGCGGGAAACACCGGAGGAGCTCATGCAAGGGCACTCCGAGGGCCCTGTGT 616
DB 634 TGTGTGCGGGAAACACCGGAGGAGCTCATGCAAGGGCACTCCGAGGGCCCTGTGT 693
QY 617 GCAGGTGATGACACTGTGCTGACGGCGGCTGTGTGAGTGGGGCGAGGGCTGTGCC 676
DB 694 GCAGGTGATGACACTGTGCTGACGGCGGCTGTGTGAGTGGGGCGAGGGCTGTGCC 753
QY 677 AGCCCAACGGGCTGGGATCTACACCGGTGTCACTACTTGAATGAGATCCACACT 736
DB 754 AGCCCAACGGGCTGGGATCTACACCGGTGTCACTACTTGAATGAGATCCACACT 813
QY 737 ATGTCCCAAAAAGCGGTGAAGCGCGCGCTGTGT 771
```

```
DB 814 ATGTCCCAAAAAGCGGTGAAGCGCGCGCTGTGT 848
RESULT 2
US-10-287-226-93
/ Sequence 93, Application US/10287226
/ Publication No. US20040086875A1
/ GENERAL INFORMATION:
/ APPLICANT: Agee, Michele L.,
/ APPLICANT: Alsobrook, John P.,
/ APPLICANT: Berghs, Constance,
/ APPLICANT: Boldog, Ference,
/ APPLICANT: Burgess, Catherine E.,
/ APPLICANT: Chant, John S.,
/ APPLICANT: Chaudhuri, Amitabha,
/ APPLICANT: DiPippo, Vincent A.,
/ APPLICANT: Edinger, Shlomit R.,
/ APPLICANT: Eilsen, Andrew,
/ APPLICANT: Ellerman, Karen,
/ APPLICANT: Gangoli, Bsha A.,
/ APPLICANT: German, Linda,
/ APPLICANT: Gerlach, Valerie,
/ APPLICANT: Gert, Weizhen,
/ APPLICANT: Kekuda, Ramesh,
/ APPLICANT: Khramtsov, Nikolai,
/ APPLICANT: Li, Li,
/ APPLICANT: Majumkar, Uriel M.,
/ APPLICANT: MacDougall, John R.,
/ APPLICANT: Mezes, Peter S.,
/ APPLICANT: Miller, Charles E.,
/ APPLICANT: Millet, Isabelle,
/ APPLICANT: Ooi, Chean Eng,
/ APPLICANT: Ort, Tatiana,
/ APPLICANT: Padigaru, Muralidhara,
/ APPLICANT: Paturajan, Meera,
/ APPLICANT: Rastelli, Luca,
/ APPLICANT: Rieger, Daniel K.,
/ APPLICANT: Rothenberg, Mark E.,
/ APPLICANT: Shenoy, Suresh G.,
/ APPLICANT: Spaderna, Steven K.,
/ APPLICANT: Spytek, Kimberley A.,
/ APPLICANT: Taupier, Jr., Raymond J.,
/ APPLICANT: Vernet, Corine A.M.,
/ APPLICANT: Zernusen, Bryan D.,
/ APPLICANT: Zhong, Mei
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-480C
/ CURRENT APPLICATION NUMBER: US/10/287,226
/ CURRENT FILING DATE: 2002-11-04
/ PRIOR APPLICATION NUMBER: 60/334,421
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,392
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/360,148
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: 60/364,000
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/404,821
/ PRIOR FILING DATE: 2002-08-20
/ PRIOR APPLICATION NUMBER: 60/334,526
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,409
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/364,227
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/334,027
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/331,641
/ PRIOR FILING DATE: 2001-11-20
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 673
/ SOFTWARE: CuroSeqList version 0.1
```

SEQ ID NO 93
LENGTH: 1145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (8)..(832)
US-10-287-226-93

Query Match 94.8%; Score 731; DB 18; Length 1145;
Best Local Similarity 98.7%; Pred. No. 2.6e-195;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	17	GAATGTCGGGGGTAGAGAGGCCCCAGAGCAAGTGGCCCTGGAGGTGAGCCCTGAGAG	76
DB	96	GCATCGTTGGGGGTAGAGAGGCCCCAGAGCAAGTGGCCCTGGAGGTGAGCCCTGAGAG	155
QY	77	TCACGGCCCACTAGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC	136
DB	156	TCACGGCCCACTAGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC	215
QY	137	TGACCGCGCGCGCGTGGGAGCCGGAAGTCAAGATCTGGCGCCCTCAGAGGTGCAAC	196
DB	216	TGACCGCGCGCGCGTGGGAGCCGGAAGTCAAGATCTGGCGCCCTCAGAGGTGCAAC	275
QY	197	TGCGGGAGCAGCAGCTTCTACTACAGACCAAGCTGCTCCCGTCAAGAGATCATCTGC	256
DB	276	TGCGGGAGCAGCAGCTTCTACTACAGACCAAGCTGCTCCCGTCAAGAGATCATCTGC	335
QY	257	ACCCAGATTCTACACCGCCGAGTCGAGAGGAGCATGCGCTGTGGAGCTGAGAGAGC	316
DB	336	ACCCAGATTCTACACCGCCGAGTCGAGAGGAGCATGCGCTGTGGAGCTGAGAGAGC	395
QY	317	CGGTGAAGGTCTCAAGCAGCTCAACAGTCAACCTGCCCCCTGCTCAAGAGACTTTC	376
DB	396	CGGTGAAGGTCTCAAGCAGCTCAACAGTCAACCTGCCCCCTGCTCAAGAGACTTTC	455
QY	377	CCCCGGGAGTCCGCTGCTGGGTCACTGCTGGGGGAGATGTGACAAATGATGAGCCCTCC	436
DB	456	CCCCGGGAGTCCGCTGCTGGGTCACTGCTGGGGGAGATGTGACAAATGATGAGCCCTCC	515
QY	437	CACCGCATTTCTCTGAAGCAGTGAAGGTCCCATATGAGAAACCAATTGTGACG	496
DB	516	CACCGCATTTCTCTGAAGCAGTGAAGGTCCCATATGAGAAACCAATTGTGACG	575
QY	497	CAAAATACCACTTGGCGCTTACACGAGAGAGCAGTCCGATCTGCTGTAAGCATGCG	556
DB	576	CAAAATACCACTTGGCGCTTACACGAGAGAGCAGTCCGATCTGCTGTAAGCATGCG	635
QY	557	TGTGTGCGGGAGAACCCGGAAGGACTCATGCGAGGGGACTCCGAGAGGCCCTGTGTGT	616
DB	636	TGTGTGCGGGAGAACCCGGAAGGACTCATGCGAGGGGACTCCGAGAGGCCCTGTGTGT	695
QY	617	GCAAGGTGAATGAGCAGTGGCTGACAGCGGGGCTGGTCACTGAGTGGGCGAGGGCTGTGCC	676
DB	696	GCAAGGTGAATGAGCAGTGGCTGACAGCGGGGCTGGTCACTGAGTGGGCGAGGGCTGTGCC	755
QY	677	AGCCCAACCGGCTGGCATCTTACACCGGTGACCTTACTTGTGACTGTGATCCACACT	736
DB	756	AGCCCAACCGGCTGGCATCTTACACCGGTGACCTTACTTGTGACTGTGATCCACACT	815
QY	737	ATGTCCCCCAAAAAGCCGTGAAGCGGCC	763
DB	816	ATGTCCCCCAAAAAGCCGTGAAGTCAAGGC	842

RESULT 3
US-10-956-157-2444
Sequence 2444, Application US/10956157
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2444
LENGTH: 1148
TYPE: DNA
ORGANISM: Homo sapiens
US-10-956-157-2444

Query Match 94.8%; Score 731; DB 21; Length 1148;
Best Local Similarity 98.7%; Pred. No. 2.6e-195;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	17	GAATGTCGGGGGTAGAGAGGCCCCAGAGCAAGTGGCCCTGGAGGTGAGCCCTGAGAG	76
DB	96	GCATCGTTGGGGGTAGAGAGGCCCCAGAGCAAGTGGCCCTGGAGGTGAGCCCTGAGAG	155
QY	77	TCACGGCCCACTAGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC	136
DB	156	TCACGGCCCACTAGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC	215
QY	137	TGACCGCGCGCGGTGGGAGCCGGAAGTCAAGATCTGGCGCCCTCAGAGGTGCAAC	196
DB	216	TGACCGCGCGCGGTGGGAGCCGGAAGTCAAGATCTGGCGCCCTCAGAGGTGCAAC	275
QY	197	TGCGGGAGCAGCAGCTTCTACTACAGACCAAGCTGCTCCCGTCAAGAGATCATCTGC	256
DB	276	TGCGGGAGCAGCAGCTTCTACTACAGACCAAGCTGCTCCCGTCAAGAGATCATCTGC	335
QY	257	ACCCAGATTCTACACCGCCGAGTCGAGAGGAGCATGCGCTGTGGAGCTGAGAGAGC	316
DB	336	ACCCAGATTCTACACCGCCGAGTCGAGAGGAGCATGCGCTGTGGAGCTGAGAGAGC	395
QY	317	CGGTGAAGGTCTCAAGCAGCTCAACAGTCAACCTGCCCCCTGCTCAAGAGACTTTC	376
DB	396	CGGTGAAGGTCTCAAGCAGCTCAACAGTCAACCTGCCCCCTGCTCAAGAGACTTTC	455
QY	377	CCCCGGGAGTCCGCTGCTGGGTCACTGCTGGGGGAGATGTGACAAATGATGAGGCCCTCC	436
DB	456	CCCCGGGAGTCCGCTGCTGGGTCACTGCTGGGGGAGATGTGACAAATGATGAGGCCCTCC	515
QY	437	CACCGCATTTCTCTGAAGCAGTGAAGGTCCCATATGAGAAACCAATTGTGACG	496
DB	516	CACCGCATTTCTCTGAAGCAGTGAAGGTCCCATATGAGAAACCAATTGTGACG	575
QY	497	CAAAATACCACTTGGCGCTTACACGAGAGAGCAGTCCGATCTGCTGTAAGCATGCG	556
DB	576	CAAAATACCACTTGGCGCTTACACGAGAGAGCAGTCCGATCTGCTGTAAGCATGCG	635
QY	557	TGTGTGCGGGAGAACCCGGAAGGACTCATGCGAGGGGACTCCGAGAGGCCCTGTGTGT	616
DB	636	TGTGTGCGGGAGAACCCGGAAGGACTCATGCGAGGGGACTCCGAGAGGCCCTGTGTGT	695
QY	617	GCAAGGTGAATGAGCAGTGGCTGACAGCGGGGCTGGTCACTGAGTGGGCGAGGGCTGTGCC	676
DB	696	GCAAGGTGAATGAGCAGTGGCTGACAGCGGGGCTGGTCACTGAGTGGGCGAGGGCTGTGCC	755
QY	677	AGCCCAACCGGCTGGCATCTTACACCGGTGACCTTACTTGTGACTGTGATCCACACT	736
DB	756	AGCCCAACCGGCTGGCATCTTACACCGGTGACCTTACTTGTGACTGTGATCCACACT	815
QY	737	ATGTCCCCCAAAAAGCCGTGAAGCGGCC	763
DB	816	ATGTCCCCCAAAAAGCCGTGAAGTCAAGGC	842

RESULT 4
US-10-956-157-1043
Sequence 1043, Application US/10956157

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (825)
US-10-287-226-91

Query Match 94.7%: Score 730.4; DB 18; Length 828;
Best Local Similarity 99.2%: Pred. No. 3.7e-195;
Matches 734; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

17 GAATGCTGGGGGTGAGAGGCCCCAGAGGCAAGTGGCCCTGAGGAGCTGAGAG 76
89 GCATGCTGGGGGTGAGAGGCCCCAGAGGCAAGTGGCCCTGAGGAGCTGAGAG 148
77 TCACAGGCCCCATCTGATGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 136
149 TCACAGGCCCCATCTGATGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 208
137 TGACCGCGCGCGGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCTCAGGGTCAAC 196
209 TGACCGCGCGCGGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCTCAGGGTCAAC 268
197 TCGGGAGAGCAGCCTCTACTACAGAGCAGCTGCTGCGGTCAAGAGATCATCTGTC 256
269 TCGGGAGAGCAGCCTCTACTACAGAGCAGCTGCTGCGGTCAAGAGATCATCTGTC 328
257 ACCCAAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGAGAGC 316
329 ACCCAAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGAGAGC 388
317 CGGTGAAGTCTCCAGCCAGTCCACAGGTCAAGCTGCGCCCTGCTCAGAGACCTTCC 376
389 CGGTGAAGTCTCCAGCCAGTCCACAGGTCAAGCTGCGCCCTGCTCAGAGACCTTCC 448
377 CCGCGGGAGTGCCTGCTGAGTCACTGAGTGGGGGAGTGGACATGATGAGCCCTCC 436
449 CCGCGGGAGTGCCTGCTGAGTCACTGAGTGGGGGAGTGGACATGATGAGCCCTCC 508
437 CACCGCATTTCTCTGAAAGCAGGTGAAGTCCCATTAATGAAAAACCATTTGTGACG 496
509 CACCGCATTTCTCTGAAAGCAGGTGAAGTCCCATTAATGAAAAACCATTTGTGACG 568
437 CAAATACCACTTGGCGCTCAACGGGAGAGAGTCCCGCATGCTGCTGAGCATGCG 556
569 CAAATACCACTTGGCGCTCAACGGGAGAGAGTCCCGCATGCTGCTGAGCATGCG 628
557 TGTGTGCGGGAGACACCGGAGGAGTCACTGCGAGGGGAGTCCGGAGGGCCCTGTGT 616
629 TGTGTGCGGGAGACACCGGAGGAGTCACTGCGAGGGGAGTCCGGAGGGCCCTGTGT 688
617 GCAAGGTGAATGCACTTGGCTGCAAGCGGGCGTGTGACCTGGAGCGAGGCTGTGCC 676
689 GCAAGGTGAATGCACTTGGCTGCAAGCGGGCGTGTGACCTGGAGCGAGGCTGTGCC 748
677 AGCCCAACCGGCTGAGTCACTACACCGGTCACCTACTACTGAGTGGATCCACACT 736
749 AGCCCAACCGGCTGAGTCACTACACCGGTCACCTACTACTGAGTGGATCCACACT 808
737 ATGTCCCAAAAAAGCGGTGA 756
809 ATGTCCCAAAAAAGCGGTGA 828

RESULT 6
US-10-723-860-6799
Sequence 6799, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
Methods for Screening for Soft Tissue Sarcoma Modulators

FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723.860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429.739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6799
LENGTH: 1334
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-6799

Query Match 94.6%: Score 729.4; DB 20; Length 1334;
Best Local Similarity 98.5%: Pred. No. 7.5e-195;
Matches 736; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

17 GAATGCTGGGGGTGAGAGGCCCCAGAGGCAAGTGGCCCTGAGGAGCTGAGAG 76
141 GCATGCTGGGGGTGAGAGGCCCCAGAGGCAAGTGGCCCTGAGGAGCTGAGAG 200
77 TCACAGGCCCCATCTGATGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 136
201 TCGGGAGAGCAGCCTCTACTACAGAGCAGCTGCTGCGGTCAAGAGATCATCTGTC 260
137 TGACCGCGCGCGGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCTCAGGGTCAAC 196
261 TGACCGCGCGCGGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCTCAGGGTCAAC 320
197 TCGGGAGAGCAGCCTCTACTACAGAGCAGCTGCTGCGGTCAAGAGATCATCTGTC 256
321 TCGGGAGAGCAGCCTCTACTACAGAGCAGCTGCTGCGGTCAAGAGATCATCTGTC 380
257 ACCCAAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGAGAGC 316
381 ACCCAAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGAGAGC 440
317 CGGTGAAGTCTCCAGCCAGTCCACAGGTCAAGCTGCGCCCTGCTCAGAGACCTTCC 376
441 CGGTGAAGTCTCCAGCCAGTCCACAGGTCAAGCTGCGCCCTGCTCAGAGACCTTCC 500
437 CACCGCATTTCTCTGAAAGCAGGTGAAGTCCCATTAATGAAAAACCATTTGTGACG 496
501 CACCGCATTTCTCTGAAAGCAGGTGAAGTCCCATTAATGAAAAACCATTTGTGACG 560
437 CAAATACCACTTGGCGCTCAACGGGAGAGAGTCCCGCATGCTGCTGAGCATGCG 556
561 CAAATACCACTTGGCGCTCAACGGGAGAGAGTCCCGCATGCTGCTGAGCATGCG 620
497 CAAATACCACTTGGCGCTCAACGGGAGAGAGTCCCGCATGCTGCTGAGCATGCG 556
621 CAAATACCACTTGGCGCTCAACGGGAGAGAGTCCCGCATGCTGCTGAGCATGCG 680
557 TGTGTGCGGGAGACACCGGAGGAGTCACTGCGAGGGGAGTCCGGAGGGCCCTGTGT 616
681 TGTGTGCGGGAGACACCGGAGGAGTCACTGCGAGGGGAGTCCGGAGGGCCCTGTGT 740
617 GCAAGGTGAATGCACTTGGCTGCAAGCGGGCGTGTGACCTGGAGCGAGGCTGTGCC 676
741 GCAAGGTGAATGCACTTGGCTGCAAGCGGGCGTGTGACCTGGAGCGAGGCTGTGCC 800
677 AGCCCAACCGGCTGAGTCACTACACCGGTCACCTACTACTGAGTGGATCCACACT 736
801 AGCCCAACCGGCTGAGTCACTACACCGGTCACCTACTACTGAGTGGATCCACACT 860
737 ATGTCCCAAAAAAGCGGTGA 763
861 ATGTCCCAAAAAAGCGGTGA 887

RESULT 7
US-09-954-456-2126
Sequence 2126, Application US/09954456

```

1 Patent No. US20020115057A1
2 GENERAL INFORMATION:
3 APPLICANT: Young, Paul
4 TITLE OR INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
5 TITLE OF INVENTION: Sets
6 FILE REFERENCE: 689290-76
7 CURRENT APPLICATION NUMBER: US/09/954, 456
8 CURRENT FILING DATE: 2001-09-18
9 PRIOR APPLICATION NUMBER: US/60/233, 617
10 PRIOR FILING DATE: 2000-09-18
11 PRIOR APPLICATION NUMBER: US/60/234, 052
12 PRIOR FILING DATE: 2000-09-20
13 PRIOR APPLICATION NUMBER: US/60/234, 923
14 PRIOR FILING DATE: 2000-09-25
15 PRIOR APPLICATION NUMBER: US/60/235, 134
16 PRIOR FILING DATE: 2000-09-25
17 PRIOR APPLICATION NUMBER: US/60/235, 637
18 PRIOR FILING DATE: 2000-09-26
19 PRIOR APPLICATION NUMBER: US/60/235, 638
20 PRIOR FILING DATE: 2000-09-26
21 PRIOR APPLICATION NUMBER: US/60/235, 711
22 PRIOR FILING DATE: 2000-09-27
23 PRIOR APPLICATION NUMBER: US/60/235, 720
24 PRIOR FILING DATE: 2000-09-27
25 PRIOR APPLICATION NUMBER: US/60/235, 840
26 PRIOR FILING DATE: 2000-09-27
27 PRIOR APPLICATION NUMBER: US/60/235, 863
28 PRIOR FILING DATE: 2000-09-27
29 NUMBER OF SEQ ID NOS: 2276
30 SOFTWARE: PatentIn version 3.0
31 SEQ ID NO 2126
32 LENGTH: 1081
33 TYPE: DNA
34 ORGANISM: Homo sapiens
35 US-09-954-456-2126

```

Query Match	Similarity	94.2%	Score 726.2	DB 9.2	Length 1081
Best Local	Similarity	98.3%	Pred. 5.8e-194		
Matches	734	Conservative	0	Mismatches	13
				Indels	0
				Gaps	0
QY	17	GAATCGTCGGGGGCTCAGAGAGCCCCCAGAGCAAGTGGCCCTCGCAGGTGAGCCTTGAGAG	76		
Db	66	GCATCGTTGGGGGTTCAGAGAGCCCCCAGAGCAAGTGGCCCTCGCAGGTGAGCCTTGAGAG	125		
QY	77	TCCACGGCCCACTGATGATGCACTTCTGCGGGGCTCCCTATCCACCCCACTGGGTGC	136		
Db	126	TCCCGACCGAGTACGATGATGCACTTCTGCGGGGCTCCCTATCCACCCCACTGGGTGC	185		
QY	137	TGACCGCGCGGGCGGTGGGACCGGACGTCACAGATCTGGCGGCTTCAGGGTGAC	196		
Db	186	TGACCGCGCGGACCTGCGGTGGGACCGGACGTCACAGATCTGGCGGCTTCAGGGTGAC	245		
QY	197	TGCGGGAGCAGACCTCTACTACAGAGCAGCTGCTCCGGTACAGACAGATCATCTGTC	256		
Db	246	TGCGGGAGCAGACCTCTACTACAGAGCAGCTGCTCCGGTACAGAGATCATCTGTC	305		
QY	257	ACCACAGTTCTACACGCGCCAGATCGGAGGGGACATGCGCTGTGGAGCTGAGAGC	316		
Db	306	ACCACAGTTCTACACGCGCCAGATCGGAGGGGACATGCGCTGTGGAGCTGAGAGC	365		
QY	317	CGGTGAAGGTTCTCAGACCAAGTCCACAGAGTCACTTCGCCCCCTGCTCAGAGACTTCC	376		
Db	366	CGGTGAAGGTTCTCAGACCAAGTCCACAGAGTCACTTCGCCCCCTGCTCAGAGACTTCC	425		
QY	377	CCCCGGGAGTCCGTCGTGGGTCACTGGCTGGGGGAGATGTGGAACAATGATAGGGCTCC	436		
Db	426	CCCCGGGAGTCCGTCGTGGGTCACTGGCTGGGGGAGATGTGGAACAATGATAGGGCTCC	485		
QY	437	CACCGCAATTTCTCTGAAGCAGGTGAAGTCCCATATGAGAAACCACTTTGTGACG	496		
Db	486	CACCGCAATTTCTCTGAAGCAGGTGAAGTCCCATATGAGAAACCACTTTGTGACG	545		
QY	497	CAAAATACACCTTTGGCGCTTACACGGGAGACAGCTCGCATGCTCGTGAACAATGC	556		

D _b	546	C A A A A T T A C C A C C T T G G C G C T T A C A C G G A G A G A A G T C C G A T C G T C C G T A G A C A C A T G C	6050
O _y	557	T G T G T C C C G G A A A C A C C C G S A G G A C T A T A T C A A G G G G A A C T C C G A A G G C C C T G G T G T	616
D _b	606	T G T G T G C C G G A A A C A C C C G A B A G A C T A T G C A M G G G G A C T C C G A A G G G C C T G G T G T	655
O _y	617	G C A A G T G A A T G G A C A C T G G C T G C A G S C G G G C G T G T G A C G C T G G G G S C G A G G C C T G T G C C C	676
D _b	666	G C A A G T G A A T G G A C A C T G G C T G C A G G G G G G C G T G T C A G C T G G G G G A A G G G C T G T G C C C	725
O _y	677	A G C C A A C C G G C C T G G A C T A C A C C C G T G C A C C T A C T A A T T T G A C T G A T C C A C A C T	736
D _b	726	A G C C A A C C G G C C T G G A C T A C A C C C G T G C A C C T A A C T T G A C T G A T C C A C A C T	785
O _y	737	A A T G C C C C A A A A A A G C C G T G A A G C G G C C	763
D _b	786	A A T G C C C C A A A A A A G C C G T A G T C A G G C	812

```

RESULT 8
US-09-960-706-680
: Sequence 680. Application US/09960706
: Publication No. US20030134280A1
: GENERAL INFORMATION:
: APPLICANT: Munger, William E.
: TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
: TITLE OF INVENTION: Gene Expression Profiles
: FILE REFERENCE: 44921-5029-01US
: CURRENT APPLICATION NUMBER: US/09/960,706
: CURRENT FILING DATE: 2001-09-24
: PRIOR APPLICATION NUMBER: 60/223,323
: PRIOR FILING DATE: 2000-08-07
: PRIOR APPLICATION NUMBER: 09/873,319
: PRIOR FILING DATE: 2001-06-05
: NUMBER OF SEQ ID NOS: 1124
: SOFTWARE: Patencin Ver. 2.1
: SEQ ID NO 680
: LENGTH: 1081
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20030134280A1 M33493
US-09-960-706-680

```

Query Match	94.2% ;	Score 726.2 ;	DB 10 ;	Length 1081 ;
Best Local Similarity	98.3% ;	Pred. No. 5.8e-194 ;		
Matches 734 ;	Conservative 0 ;	Mismatches 13 ;	Indels 0 ;	Gaps 0 ;
QY	17	GAATCGTCGGGGGTCAGAGAGCCCCAGAGCAAGTGGCCCTTGACAGGTGACCTTGAGAG	76	
Db	66	GCATCGTTGGGGGTCAGAGAGCCCCAGAGCAAGTGGCCCTTGACAGGTGACCTTGAGAG	125	
QY	77	TTCACGGGCCCACTAGATGATGACTTCTGCGGGGGCTCCCTCATCACCCCAAGTGGGTGC	136	
Db	126	TCCCGCAGCCCACTAGATGATGACTTCTGCGGGGGCTCCCTCATCACCCCAAGTGGGTGC	185	
QY	137	TGACCGCGGGGGGTGGTGGGACCGGACGTCAGAGATCTGGCCGCCCTCAGGGGTGCAAC	196	
Db	186	TGACCGCGGCGCACTGGTGGGACCGGACGTCAGAGATCTGGCCGCCCTCAGGGGTGCAAC	245	
QY	197	TGCGGGAGCAGCACCTCTACTACAGGACCAAGCTGTGCGGTGACAGAGATCATCTGTGC	256	
Db	246	TGCGGGAGCAGCACCTCTACTACAGGACCAAGCTGTGCGGTGACAGAGATCATCTGTGC	305	
QY	257	ACCACACGTTCTACACCGCCCAAGTCGAGCGGACATGCGCCCTGTGAGCTGAGAGAGC	316	
Db	306	ACCACACGTTCTACACCGCCCAAGTCGAGCGGACATGCGCCCTGTGAGCTGAGAGAGC	365	
QY	317	CGGTGAAGGTCCTCAGGCAAGTCACAGGTCACCCCTGCGCCCTCAGAGACCTTCC	376	
Db	366	CGGTGAAGGTCCTCAGGCAAGTCACAGGTCACCCCTGCGCCCTCAGAGACCTTCC	425	

Qy	377	CCCCGGGGAAGCGCTGCTCTGGATCACTGCGCTGGGGCGATGTGGACAATGATAGGCGCTCC	436
Db	426	CCCCGGGGAAGCGCTGCTGGATCACTGCGCTGGGGCGATGTGGACAATGATAGGCGCTCC	485
Qy	437	CACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATTAATGAAAAACCAATTTGTACG	496
Db	486	CACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATTAATGAAAAACCAATTTGTACG	545
Qy	497	CAAAATTCACCTTTGGCGCTTACACGGGAGACAGACTCCGATCGTCCGTGAACACATGC	556
Db	546	CAAAATTCACCTTTGGCGCTTACACGGGAGAGAGAGTCGGATCGTCCGTGAACACATGC	605
Qy	557	TGTTGTGCGGGGAACACCCGGAGGGATCTATGCGACAGGCGACCTCCGGAGGGCCCTGTGTT	616
Db	606	TGTTGTGCGGGGAACACCCGGAGGGATCTATGCGACAGGCGACTTCGGAGAGGCCCTTGTGTT	665
Qy	617	GCAAGGTGAATGGCACCTGCTGTCAGGCGGGGCTGTGATCAGCTGGGGCGAGGGCTGTGCC	676
Db	666	GCAAGGTGAATGGCACCTGCTGTCAGGCGGGGCTGTGATCAGCTGGGGCGAGGGCTGTGCC	725
Qy	677	AGCCCAACCGGCTCGGCACTTACACCCCGTGTCACTTACTTGGACTGGATTCACCACT	726
Db	726	AGCCCAACCGGCTCGGCACTTACACCCCGTGTCACTTACTTGGACTGGATTCACCACT	785
Qy	737	ATGTGCCCAAAAAGCGGTGAAGGCGCC	763
Db	786	ATGTGCCCAAAAAGCGGTGAAGGCGCC	812

RESULT 9
US-09-873-319-427

```

Sequence 427, Application US/09873319A
Publication No. US20030134324A1
GENERAL INFORMATION:
APPLICANT: Munger, William E.
APPLICANT: Kulkarni, Prakash
APPLICANT: Getzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
FILE REFERENCE: 44921-5029-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 427
LENGTH: 1081
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20030134324A1 M33493
US-09-873-319-427

```

Query Match	94.2%	Score	726.2	DB	10	Length	1081
Best Local Similarity	98.3%	Pred. NO.	5.8e-194				
Matches	734	Conservative	0	Mismatches	13	Indels	0
						Gaps	0

Oy	77	TCACGGCCCATATCTGGATGCACTTTCGGGGGGCTCCCTCATCCACCCCAAGTGGGTGC	136
Db	66	GCAATCTTGGGGGGTCAAGAGAGCCCCCAAGAGCAATGTGGCCCTTGGCAGGTGAGCCTGAGAG	125
Oy	17	GAATCTCTGGGGGGTCAAGAGAGCCCCCAAGAGCAATGTGGCCCTTGGCAGGTGAGCCTGAGAG	76
Oy	137	TGACCGCCGGCGGTGCTGTGGAGCCGGAGCGTCAAGGATCTGGCCGCTTCAGGGTGCAC	198
Db	186	TGACCGGAGCGCACTGTGTGGAGCCGGAGCGTCAAGGATCTGGCCGCTTCAGGGTGCAC	245
Oy	197	TGCGGAGCGACACTTTCATTCACAGACCAAGCTGTCCGGTTCAGCAGATCATCTGTC	256

Db	246	TTGGGGAGCGACGCTCTACTACAGGACGAGTGTGGCGGTGACAGAGGATCATCTGTGC	305
OY	257	ACCCACAGTTCTACACCGCCAGATGGAGCGGACATGGCCCTGTCTGAGCTGGAGAGGC	316
Db	306	ACCCACAGTTCTACACCGCCAGATGGAGCGGACATGGCCCTGTCTGAGCTGGAGAGGC	365
OY	317	CGGTGAAGGTCTCCAGCGCAGTCCACACGGTCAACCTGGCCCTGCTCAGAGACCTTCC	376
Db	366	CGGTGAAGGTCTCCAGCGCAGTCCACACGGTCAACCTGGCCCTGCTCAGAGACCTTCC	425
OY	377	CCCCGGAGATGCCGTCTGGGTCACTGCGTGGGGCGATGTGCAATGATGAGCGCTTC	436
Db	426	CCCCGGAGATGCCGTCTGGGTCACTGCGTGGGGCGATGTGCAATGATGAGCGCTTC	485
OY	437	CACCGCATTTCTCTGAAGCAGGTGAAGSTCCCCATATGAAAAACCATTTGTGACG	496
Db	486	CACCGCATTTCTCTGAAGCAGGTGAAGSTCCCCATATGAAAAACCATTTGTGACG	545
OY	497	CAAAATACCACTTTGGCGCTACACCGGAGAGCAGCGTCCGATCGTCCGTGACGATGC	556
Db	546	CAAAATACCACTTTGGCGCTACACCGGAGAGCAGCGTCCGATCGTCCGTGACGATGC	605
OY	557	TGTGTGCCGGGAAACCCCGGAGGGAATCTATGCCAGGGCCATCTCCGAGGGCCCCGTGTGT	616
Db	606	TGTGTGCCGGGAAACCCCGGAGGGAATCTATGCCAGGGCCATCTCCGAGGGCCCCGTGTGT	665
OY	617	GCAAGGTGAATGACACCTGGCTTGCAGGCGGGCGTGTGAGCTGGGGCGAGGGCTGTGCC	676
Db	666	GCAAGGTGAATGACACCTGGCTTGCAGGCGGGCGTGTGAGCTGGGGCGAGGGCTGTGCC	725
OY	677	AGCCCAACCGGCTGGGATCTACACCCGTGTCACTTACTTTGGACTGGAATCCACACT	736
Db	726	AGCCCAACCGGCTGGGATCTACACCCGTGTCACTTACTTTGGACTGGAATCCACACT	785
OY	737	ATGTCCCCAANAAGCGGTGAAGGGGC	763
Db	786	ATGTCCCCAANAAGCGGTGAAGGGGC	812

RESULT 10
US-09-873-367C-155

```

: Sequence 155, Application US/09873367C
: Publication No. US20030165839A1
: GENERAL INFORMATION:
: APPLICANT: Young, Paul
: APPLICANT: Soppet, Daniel
: APPLICANT: Endress, Gregory
: APPLICANT: Augustus, Meena
: APPLICANT: Ebner, Reinhard
: APPLICANT: Carter, Kenneth
: TITLE OR INVENTION: Cancer Gene Determination and Therapeutic Screening Using
: TITLE OR INVENTION: Signature Gene Sets
: FILE REFERENCE: 689290-64
: CURRENT APPLICATION NUMBER: US/09/873,367C
: CURRENT FILING DATE: 2003-04-29
: PRIOR APPLICATION NUMBER: U.S. 60/236,891
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: U.S. 60/236,842
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: U.S. 60/244,867
: PRIOR FILING DATE: 2000-11-01
: PRIOR APPLICATION NUMBER: U.S. 60/245,084
: PRIOR FILING DATE: 2000-11-01
: NUMBER OF SEQ ID NOS: 1067
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 155
: LENGTH: 1081
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-873-367C-155

```

Query Match 94.2%; Score 726.2; DB 10; Length 1081;

Best Local Similarity 98.3%; Pred. No. 5.8e-194;
Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY	17	GAATCGTCGGGGGTCAGAGAGCCGCCCAAGAGCAAGTGAGCCCTGGCAGGTAGCTGAGAG	76
Db	66	GCATCTGTTGGGGGTTCAGAGAGCCGCCCAAGAGCAAGTGAGCCCTGGCAGGTAGCTGAGAG	125
QY	77	TTCAAGGCGCCATCTGATGATGACTTTCTGCGGGGCTCCCTCATCAACCCCAAGTGAGTGC	136
Db	126	TTCCGAGACCGATCTGATGATGACTTTCTGCGGGGCTCCCTCATCAACCCCAAGTGAGTGC	185
QY	137	TGACCGCGCGGGCGTGGGAGCCGAGACGCTCAAGGATCTGGGCGGCCCTGAGGTGTAAC	196
Db	186	TGACCGCGCGGACACTGGGTGGAGCCGAGACGCTCAAGGATCTGGGCGGCCCTGAGGTGTAAC	245
QY	197	TGCGGAGACAGACCTCTACTACAGAGAACCAAGCTGTCCGGTTCAGAGGATCATCGTGC	256
Db	246	TGCGGAGACAGACCTCTACTACAGAGAACCAAGCTGTCCGGTTCAGAGGATCATCGTGC	305
QY	257	ACCCACAGTTTACACCGGCCAGATGGAGGGGAGCATGGCGCTGTGGAGACTGAGAGAGC	316
Db	306	ACCCACAGTTTACACCGGCCAGATGGAGGGGAGCATGGCGCTGTGGAGACTGAGAGAGC	365
QY	317	CGGTGAAGGCTTCAGGCAACGTCCACAACGCTCAACCTTCCCTGTCTCAGAGACCTTCC	376
Db	366	CGGTGAAGGCTTCAGGCAACGTCCACAACGCTCAACCTTCCCTGTCTCAGAGACCTTCC	425
QY	377	CCCCGGGAGTCCGCTGTGGGTCACTGGCTGGGGCCATGTGGACATGATGAGCCCTCC	436
Db	426	CCCCGGGAGTCCGCTGTGGGTCACTGGCTGGGGCCATGTGGACATGATGAGCCCTCC	485
QY	437	CACCGCCATTCTCTGAGAGAGGTGAAGGTCCCATTAATGAGAAACCACATTTGTGAGC	496
Db	486	CACCGCCATTCTCTGAGAGAGGTGAAGGTCCCATTAATGAGAAACCACATTTGTGAGC	545
QY	497	CAAAATACCACTTTGGCGGCTTACACGGGAGACGACGTCGCGATGCTCGTACGACATGC	556
Db	546	CAAAATACCACTTTGGCGGCTTACACGGGAGACGACGTCGCGATGCTCGTACGACATGC	605
QY	557	TGTTGTCGGGGAACACCCGAGAGGATCTATGCGAGGGCGACTCCGGAGGGCCCTGTGTGT	616
Db	606	TGTTGTCGGGGAACACCCGAGAGGATCTATGCGAGGGCGACTCCGGAGGGCCCTGTGTGT	665
QY	617	GCAAGGTGAATGGCACTTGCTGCAAGGCGGGCGTGTCACTGGGGCGAGAGGCTGTGTGCC	676
Db	666	GCAAGGTGAATGGCACTTGCTGCAAGGCGGGCGTGTCACTGGGGCGAGAGGCTGTGTGCC	725
QY	677	AGCCCAACCGGCGCTGGGATCTAACCCGGTGTCACTACTTGGACTGGATCCACACT	736
Db	726	AGCCCAACCGGCGCTGGGATCTAACCCGGTGTCACTACTTGGACTGGATCCACACT	785
QY	737	ATGTCCCAAAAGAACCGTGAAGCGGCC	763
Db	786	ATGTCCCAAAAGAACCGTGAAGTACGGC	812
RESULT 11			
US-09-873-367C-714			
Sequence 714, Application US/09873367C			
Publication No. US20030165839A1			
GENERAL INFORMATION:			
APPLICANT: Young, Paul			
APPLICANT: Soppet, Daniel			
APPLICANT: Endress, Gregory			
APPLICANT: Augustus, Meena			
APPLICANT: Ebner, Reinhard			
APPLICANT: Carter, Kenneth			
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using			
FILE REFERENCE: 689290-64			
CURRENT APPLICATION NUMBER: US/09/873.367C			
CURRENT FILING DATE: 2003-04-29			
PRIOR APPLICATION NUMBER: U.S. 60/236,891			

```

/ PRIOR FILING DATE: 2000-09-29      60/236,842
/ PRIOR APPLICATION NUMBER: U.S.
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: U.S. 60/244,867
/ PRIOR FILING DATE: 2000-11-01
/ PRIOR APPLICATION NUMBER: U.S. 60/245,084
/ PRIOR FILING DATE: 2000-11-01
/ NUMBER OF SEQ ID NOS: 1067
/ SOFTWARE: patentIn version 3.0
/ SEQ ID NO 714
/ LENGTH: 1081
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-873-367C-714

```

Query Match	94.2%	Score 726.2;	DB 10;	Length 1081;
Best Local Similarity	98.3%	Pred. No. 5.8e-194;		
Matches 734;	Conservative	0;	Mismatches 13;	Indels 0;
				Gaps 0;

QY	17	GAATCGTCGGGGGGTCAAGAGAGGCCCCAGAGACAATGGACCTGGCAGGTGACCTGAGAG	76
Db	66	GCATCGTTGGGGGTCAAGAGGCCCCAGAGACAATGGACCTGGCAGGTGACCTGAGAG	122
QY	77	TCCAGCGCCCATACTGATGATGCACTTCTGCGGGGGCTCCCTGATCCACCCCAAGTGGTGCC	136
Db	126	TCCGGGACCGGATATCTGGATGCACTTCTGCGGGGGCTCCCTATCCACCCCAAGTGGTGCC	188
QY	137	TGACCGCCGCGGCGGTGCGTGGGACCGGACGTGACAGGATCTTGACCGCCCTCAGGGTGCAC	196
Db	186	TGACCCCAACCGCACTGCGTGGGACCGGACGTGACAGGATCTTGACCGCCCTCAGGGTGCAC	244
QY	197	TGGGGGAGAGACGCTCTACACAGAGACAGAGCTGCGCGGTGACAGAGATCAATCGTGC	256
Db	246	TGGGGGAGAGACGCTCTACACAGAGACAGAGCTGCGCGGTGACAGAGATCAATCGTGC	308
QY	257	ACCACAGTTCTACACCGGCCAGATCGAGGGGACATGCGCCTCTGGAGCTGAGAGAC	318
Db	306	ACCACAGTTCTACACCGGCCAGATCGAGGGGACATGCGCCTCTGGAGCTGAGAGAC	366
QY	317	CGGTGAAGGTCTCCAGCCACGTCACACAGGTCACTGACCTGCCCTTGCTCAGAGACTTTCC	376
Db	366	CGGTGAAGGTCTCCAGCCACGTCACACAGGTCACTGACCTGCCCTTGCTCAGAGACTTTCC	428
QY	377	CCCCGGGAGATGCGGTGCTGGGTCACTGGCTGGGGGGAGATGAGACAAATGAGAGGCTCC	438
Db	426	CCCCGGGAGATGCGGTGCTGGGTCACTGGCTGGGGGGAGATGAGACAAATGAGAGGCTCC	488
QY	437	CACCGCATTTCTCTGAAAGCAGGTGAAGGTCCCATATGAGAAAAACCATTTGTGACG	496
Db	486	CACCGCATTTCTCTGAAAGCAGGTGAAGGTCCCATATGAGAAAAACCATTTGTGACG	548
QY	497	CAAAATACCACTTGGCGCTTACACGCGSAGACGAGCTGCGATGTCCGTGACGACATGC	556
Db	546	CAAAATACCACTTGGCGCTTACACGCGSAGACGAGCTGCGATGTCCGTGACGACATGC	608
QY	557	TGTGTGTCGGGAGACACCCGGAGGGACATATGCTCAGGGGGAATCCCGAGAGGCCCTTGATGT	616
Db	606	TGTGTGTCGGGAGACACCCGGAGGGACATATGCTCAGGGGGAATCCCGAGAGGCCCTTGATGT	668
QY	617	GCAAGGTGAATGGACCTGCGTGCAGCGGGCGCGCTGTGACGTGGGGGAGAGGCTGTGCC	676
Db	666	GCAAGGTGAATGGACCTGCGTGCAGCGGGCGCGCTGTGACGTGGGGGAGAGGCTGTGCC	728
QY	677	AGCCCAACCGGCTTGGCATTTACACCCGCTGTCACTTACTTGGAGCTGATCCACACT	736
Db	726	AGCCCAACCGGCTTGGCATTTACACCCGCTGTCACTTACTTGGAGCTGATCCACACT	788
QY	737	ATGTGCCCCAAAAAGCCGTGAAGCGGCC	763
Db	786	ATGTGCCCCAAAAAGCCGTGAAGCTCAGGC	812

RESULT 12

Db 126 TCCGCCACCGATCTGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCAAGTGGTGC 185
QY 137 TGAACCCGCGCGGTGCTGAGGAGCCGAGCGTCAAGATCTGGCCGCCCTCAGGGTCAAC 196
Db 186 TGACCGGAGCGCACTGGGTGGGACCGGAGCGTCAAGGATCTGGCCGCCCTCAGGGTCAAC 245
QY 197 TGGGGGAGCGACCTCTTACTACAGACCAAGTGTGCTGGGCTGAGAGATCATGTGC 256
Db 246 TGGGGGAGCGACCTCTTACTACAGACCAAGTGTGCTGGGCTGAGAGATCATGTGC 305
QY 257 ACCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGTGAGACTGAGAGAG 316
Db 306 ACCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGTGAGACTGAGAGAG 365
QY 317 CGGTGAAGTCTTCAAGCAGCTCAACCGGTCAACCCCTGCCCTCCTCAGAGACCTTCC 376
Db 366 CGGTGAAGTCTTCAAGCAGCTCAACCGGTCAACCCCTGCCCTCCTCAGAGACCTTCC 425
QY 377 CCGCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGACATGATGAGCGCTCC 436
Db 426 CCGCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGACATGATGAGCGCTCC 485
QY 437 CACCGCATTTCTCTGAAAGCAGGTGAAGTCCCAATGAAACCAATTTGTGACG 496
Db 486 CACCGCATTTCTCTGAAAGCAGGTGAAGTCCCAATGAAACCAATTTGTGACG 545
QY 497 CAAATATCAACTTGGGCGCTTACACGGAGACGACGTCCGATGTCCTGTGACGACATGC 556
Db 546 CAAATATCAACTTGGGCGCTTACACGGAGACGACGTCCGATGTCCTGTGACGACATGC 605
QY 557 TGTGTGCGGGGAAACCCCGAGGGAGCTCATGSCAGGGCGCATCCCGAGGGGCCCTGGTGT 616
Db 606 TGTGTGCGGGGAAACCCCGAGGGAGCTCATGSCAGGGCGCATCCCGAGGGGCCCTGGTGT 665
QY 617 GCAAGGTGATGSCACTGTGCTGACGAGCGGGCGTGTGACTGAGGGCGAGGGCTGTGCC 676
Db 666 GCAAGGTGATGSCACTGTGCTGACGAGCGGGCGTGTGACTGAGGGCGAGGGCTGTGCC 725
QY 677 AGCCCAACCGGCTGGGCTTACACCGGTGTACCTTACTTGTGACTGAGTCAACACT 736
Db 726 AGCCCAACCGGCTGGGCTTACACCGGTGTACCTTACTTGTGACTGAGTCAACACT 785
QY 737 ATGTCCCAAAAAAGCGGTGAAGCGGCC 763
Db 786 ATGTCCCAAAAAAGCGGTGAAGCGGCC 812

RESULT 14
US-10-843-641A-5153
; Sequence 5153, Application US/10843641A
; Publication No. US2005006454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007

; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 5153
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5153

Query Match 94.2%; Score 726.2; DB 21; Length 1081;
Best Local Similarity 98.3%; Pred. No. 5.8e-194;
Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 GATGTGCGGGGTGAGAGGCCCCAGAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
Db 66 GCATGCTGGGGGTGAGAGGCCCCAGAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 125
QY 77 TCCAGGGCCATCTGAGATGACCTTCTGGGGGGCTCCCTCATCCACCCCAAGTGGTGC 136
Db 126 TCCAGGACCGATCTGAGATGACCTTCTGGGGGGCTCCCTCATCCACCCCAAGTGGTGC 185
QY 137 TGACCGCGCGCGGTGCTGAGAGCCGAGCGTCAAGATCTGAGCGCCCTCAGGGTCAAC 196
Db 186 TGACCGCGCGCGGTGCTGAGAGCCGAGCGTCAAGATCTGAGCGCCCTCAGGGTCAAC 245
QY 197 TGGGGGAGCGACCTCTTACTACAGACCAAGTGTGCTGGGCTGAGAGATCATGTGC 256
Db 246 TGGGGGAGCGACCTCTTACTACAGACCAAGTGTGCTGGGCTGAGAGATCATGTGC 305
QY 257 ACCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGTGAGACTGAGAGAG 316
Db 306 ACCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGTGAGACTGAGAGAG 365
QY 317 CGGTGAAGTCTTCAAGCAGCTCAACCGGTCAACCCCTGCCCTCCTCAGAGACCTTCC 376
Db 366 CGGTGAAGTCTTCAAGCAGCTCAACCGGTCAACCCCTGCCCTCCTCAGAGACCTTCC 425
QY 377 CCGCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGACATGATGAGCGCTCC 436
Db 426 CCGCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGACATGATGAGCGCTCC 485
QY 437 CACCGCATTTCTCTGAAAGCAGGTGAAGTCCCAATGAAACCAATTTGTGACG 496
Db 486 CACCGCATTTCTCTGAAAGCAGGTGAAGTCCCAATGAAACCAATTTGTGACG 545
QY 497 CAAATATCAACTTGGGCGCTTACACGGAGACGACGTCCGATGTCCTGTGACGACATGC 556
Db 546 CAAATATCAACTTGGGCGCTTACACGGAGACGACGTCCGATGTCCTGTGACGACATGC 605
QY 557 TGTGTGCGGGGAAACCCCGAGGGAGCTCATGSCAGGGCGATCCCGAGGGGCCCTGGTGT 616
Db 606 TGTGTGCGGGGAAACCCCGAGGGAGCTCATGSCAGGGCGATCCCGAGGGGCCCTGGTGT 665
QY 617 GCAAGGTGATGSCACTGTGCTGACGAGCGGGCGTGTGACTGAGGGCGAGGGCTGTGCC 676
Db 666 GCAAGGTGATGSCACTGTGCTGACGAGCGGGCGTGTGACTGAGGGCGAGGGCTGTGCC 725
QY 677 AGCCCAACCGGCTGGGCTTACACCGGTGTACCTTACTTGTGACTGAGTCAACACT 736
Db 726 AGCCCAACCGGCTGGGCTTACACCGGTGTACCTTACTTGTGACTGAGTCAACACT 785
QY 737 ATGTCCCAAAAAAGCGGTGAAGCGGCC 763
Db 786 ATGTCCCAAAAAAGCGGTGAAGCGGCC 812

RESULT 15
US-10-275-505-27

Sequence 27, Application US/10275505
Publication No. US20040081961A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: DELEGEANNE, Angelo M.; LAL, Preeti G.
APPLICANT: HAPALIA, April J.A.; PATTERSON, Chandra
APPLICANT: WALIA, Narinder K.; KEARNEY, Liam
APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
APPLICANT: YAO, Monique G.; BAUGHN, Marian R.
APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.
APPLICANT: YANG, Junming; HERNANDEZ, Roberto
APPLICANT: POLICKY, Jennifer L.; LU, Dyung Anna M.
APPLICANT: REDDY, Roopa M.; YUE, Henry
APPLICANT: TANG, Y. Tom
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PI-0085 USN
CURRENT APPLICATION NUMBER: US/10/275,505
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: PCT/US01/14651
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/209,402
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/207,477
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/205,803
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 60/203,566
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/202,082
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 27
LENGTH: 2662
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7472460CBI
US-10-275-505-27

Query Match 93.2%; Score 718.2; DB 18; Length 2662;

Beet Local Similarity 98.2%; Pred. No. 1.1e-191;

Matches 726; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 GAATGTCGGGGGTGAGAGGCCCCAGAGGCAAGTGAGCCCTGGCAGATGAGCTGAGAG 76
DB 699 GCATGTTGGGGGTGAGAGGCCCCAGAGGCAAGTGAGCCCTGGCAGATGAGCTGAGAG 758
QY 77 TCACGAGCCCACTGATGCACTTCTGCGGGGCTCCCTCATCAACCCCAAGTGGTGC 136
DB 759 TCCGGGACCGATGATGATGCACTTCTGCGGGGCTCCCTCATCAACCCCAAGTGGTGC 818
QY 137 TGACCGCGCGCGGCGTGGGAGACCGGAGCTCAAGGATGAGCCCGCTCAGGGTGAAC 196
DB 819 TGACCGCAGCGCATGCGGGAGCCGAGACGTCAAGGATGAGCCCGCTCAGGGTGAAC 878
QY 197 TCGGGAGAGCAGCCTCTACTACAGAGACAGCTGCTGCGGTGACAGAGATCATCTGTC 256
DB 879 TCGGGAGAGCAGCCTCTACTACAGAGACAGCTGCTGCGGTGACAGAGATCATCTGTC 938
QY 257 ACCCAGATTCTACACCGCGCCAGATGAGCGGACATGCGCTGCTGAGCTGAGAGAGC 316
DB 939 ACCCAGATTCTACACCGCGCCAGATGAGCGGACATGCGCTGCTGAGCTGAGAGAGC 998
QY 317 CGATGAAGGTCTCAGCGCAGCTCAACAGGATCAACCTGCGCCCTGCTCAGAGACTTTC 376
DB 999 CGATGAAGGTCTCAGCGCAGCTCAACAGGATCAACCTGCGCCCTGCTCAGAGACTTTC 1058
QY 377 CCGCGGAGATGCGCTGCTGAGCTCACTGCTGCGGGCGATGTGACAATGATGAGCGCTTC 436
DB 1059 CCGCGGAGATGCGCTGCTGAGCTCACTGCTGCGGGCGATGTGACAATGATGAGCGCTTC 1118

QY 437 CACCGCATTTCTCTGAGCAGGTGAAGGTCCTCATTAATGAGAAACACATTGTCAGC 496
DB 1119 CACCGCATTTCTCTGAGCAGGTGAAGGTCCTCATTAATGAGAAACACATTGTCAGC 1178
QY 497 CAAATACCACTTGGCGCTTACACGGGAGACAGCTCCGATGTCGCTGACACATGC 556
DB 1179 CAAATACCACTTGGCGCTTACACGGGAGACAGCTCCGATGTCGCTGACACATGC 1238
QY 557 TGTGTGCGGGAGACACCGGAGGAGCTCATGCAAGGCGACTCCGAGAGGCTGCTGT 616
DB 1239 TGTGTGCGGGAGACACCGGAGGAGCTCATGCAAGGCGACTCCGAGAGGCTGCTGT 1298
QY 617 GCAAGGTGAATGAGCAGCTGCTGCAAGGCGGCGTGTCAAGTGGGAGAGGCTGTGCC 676
DB 1299 GCAAGGTGAATGAGCAGCTGCTGCAAGGCGGCGTGTGTCAAGTGGGAGAGGCTGTGCC 1358
QY 677 AGCCCAACCGGCTGAGATCTACACCGGTGTCACTTACTTGAATGATGACGACT 736
DB 1359 AGCCCAACCGGCTGAGATCTACACCGGTGTCACTTACTTGAATGATGACGACT 1418
QY 737 ATGTCCCAAAAAGCCGTG 755
DB 1419 ATGTCCCAAAAAGCCGTG 1437

Search completed: August 27, 2005, 21:22:53
Job time : 630 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 18:58:19 ; Search time 188 Seconds
(without alignments)
6710.475 Million cell updates/sec

Title: US-09-598-982C-20

Perfect score: 771
Sequence: 1 gggccctcgagaaagaat.....cgtgagcgccgcgcgtcgt 771

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCRTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	764.6	99.2	771	3	US-09-079-970A-4
2	731	94.8	1128	2	US-09-016-366A-20
3	731	94.8	1128	2	US-08-978-404B-15
4	731	94.8	1137	2	US-09-016-366A-18
5	731	94.8	1137	2	US-08-978-404B-13
6	728.6	94.5	735	3	US-09-079-970A-1
7	726.2	94.2	1081	2	US-09-016-366A-22
8	726.2	94.2	1081	2	US-08-978-404B-17
9	726.2	94.2	1081	4	US-09-917-254-50
10	686.2	89.0	1154	2	US-09-016-366A-16
11	686.2	89.0	1154	2	US-08-978-404B-11
12	477.2	61.9	1219	2	US-08-978-404B-7
13	469.6	60.9	1108	2	US-09-016-366A-14
14	469.6	60.9	1108	2	US-08-978-404B-20
15	463	60.1	1031	2	US-08-978-404B-1
16	445.6	57.8	1103	2	US-09-016-366A-24
17	444	57.6	1097	2	US-08-978-404B-4
18	371	48.1	1225	3	US-08-845-998-3
19	371	48.1	1225	3	US-09-206-537-3
20	371	48.1	1225	3	US-09-430-854-3
21	369.4	47.9	2218	2	US-08-845-998-5
22	369.4	47.9	2218	3	US-09-206-537-5
23	369.4	47.9	2218	3	US-09-430-854-5
24	271.8	35.3	1095	2	US-08-978-404B-9
25	201.4	26.1	1110	4	US-09-023-942A-30
26	201.4	26.1	1110	3	US-09-386-653A-1
27	199.8	25.9	1212	4	US-09-620-312D-431

28	193.8	25.1	1130	3	US-09-386-653A-8	Sequence 8, Appl
29	187.8	24.4	1613	4	US-09-387-375-1	Sequence 1, Appl
30	187.8	24.4	1613	4	US-10-041-400A-1	Sequence 1, Appl
31	187.8	24.4	1613	4	US-10-042-091A-1	Sequence 8, Appl
32	181.2	23.5	1130	4	US-09-387-375-8	Sequence 8, Appl
33	181.2	23.5	1130	4	US-10-041-400A-8	Sequence 8, Appl
34	181.2	23.5	1130	4	US-10-042-091A-8	Sequence 8, Appl
35	153	19.8	3757	2	US-09-016-366A-13	Sequence 13, Appl
36	153	19.8	3757	2	US-08-978-404B-19	Sequence 19, Appl
37	152	19.7	933	4	US-09-023-942A-29	Sequence 29, Appl
38	143.8	18.7	2397	2	US-08-978-404B-2	Sequence 2, Appl
39	140.6	18.2	1142	3	US-09-386-642-8	Sequence 7, Appl
40	140.6	18.2	1142	3	US-09-386-642-7	Sequence 7, Appl
41	132.2	17.1	1154	4	US-09-636-382A-1	Sequence 1, Appl
42	131.2	17.0	1165	4	US-09-023-942A-28	Sequence 28, Appl
43	131.2	17.0	1378	4	US-09-907-794A-262	Sequence 262, App
44	131.2	17.0	1378	4	US-09-905-125A-262	Sequence 262, App
45	131.2	17.0	1378	4	US-09-902-775A-262	Sequence 262, App

ALIGNMENTS

RESULT 1
US-09-079-970A-4
Sequence 4, Application US/09079970A
Patent No. 6274366
GENERAL INFORMATION:
APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Intellectual Property Department
STREET: 8000 Exceltior Drive, Suite 401
CITY: Madison
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34506.073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 7..753
FEATURE:
NAME/KEY: misc_signal

LOCATION: 7..18
US-09-079-970A-4

Query Match 99.2%; Score 764.6; DB 3; Length 771;
Best Local Similarity 99.5%; Pred. No. 1.4e-169;
Matches 767; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 GGGGCCCCGAGAGAAATCGTCGGGGGGTCAGAGAGCCCCCGAGAGCAAGTGGCCCTGG 60
DB 1 GGGGCCCCGAGAGAAATCGTCGGGGGGTCAGAGAGCCCCCGAGAGCAAGTGGCCCTGG 60
QY 61 CAGGTAGCCCTGAGAGTCCACCGGCCATATCTGATGCACTTCTGCGGGGCTCCCTCATC 120
DB 61 CAGGTAGCCCTGAGAGTCCACCGGCCATATCTGATGCACTTCTGCGGGGCTCCCTCATC 120
QY 121 CACCCCACTGAGGTGCTGACCCCGGGGGCTGCTGGAGACCGGACCTCAAGATCTGGGC 180
DB 121 CACCCCACTGAGGTGCTGACCCCGGGGGCTGCTGGAGACCGGACCTCAAGATCTGGGC 180
QY 181 GGCCTCAGGGTGCACTGCGGGAGAGCACTCTACTACAGAGACAGCTGCTGGCCGCTC 240
DB 181 GGCCTCAGGGTGCACTGCGGGAGAGCACTCTACTACAGAGACAGCTGCTGGCCGCTC 240
QY 241 AGCAGATATCATGTGACACCCACAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTG 300
DB 241 AGCAGATATCATGTGACACCCACAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTG 300
QY 301 CTGGAGCTGAGAGAGCGCGGTGAAAGTCTCCAGGCACTGTCACACGCTGCCCCCT 360
DB 301 CTGGAGCTGAGAGAGCGCGGTGAAAGTCTCCAGGCACTGTCACACGCTGCCCCCT 360
QY 361 GCCTCAGAGACTTCCCGCCGGGGATGCGGTGCGGTCACTGCTGAGGAGCATGAGAC 420
DB 361 GCCTCAGAGACTTCCCGCCGGGGATGCGGTGCGGTCACTGCTGAGGAGCATGAGAC 420
QY 421 AATGATGAGCGCTTCCACCGCATTTCTCTGAGACAGGTGAAGTCCCATATGAGAA 480
DB 421 AATGATGAGCGCTTCCACCGCATTTCTCTGAGAGCAAGTGAAGTCCCATATGAGAA 480
QY 481 AACCAATTTGTGACCGCAAAATACCACTTTGGGCTTACACCGGAGACAGACGTCGCGATC 540
DB 481 AACCAATTTGTGACCGCAAAATACCACTTTGGGCTTACACCGGAGACAGACGTCGCGATC 540
QY 541 GTCCGTCAGACATGCTGTGTGCGGGGAAACACCGGAGGAACTCATGCCAGGCGACTCC 600
DB 541 GTCCGTCAGACATGCTGTGTGCGGGGAAACACCGGAGGAACTCATGCCAGGCGACTCC 600
QY 601 GAGAGGCCCCGTGTGTGCAAGGTGAATGCACTGCTGAGCGGGCGTGTCAAGCTGG 660
DB 601 GAGAGGCCCCGTGTGTGCAAGGTGAATGCACTGCTGAGCGGGCGTGTCAAGCTGG 660
QY 661 GGGAGAGGCTGTGCGCGAGCCCAACCGGCTGGGATCTACACCGGTCTCACTACTTGG 720
DB 661 GGGAGAGGCTGTGCGCGAGCCCAACCGGCTGGGATCTACACCGGTCTCACTACTTGG 720
QY 721 GACTGATCCACCACTATGTCCCAAAAAGCGGTGAAGGCGCGCGTGTGT 771
DB 721 GACTGATCCACCACTATGTCCCAAAAAGCGGTGAAGGCGCGCGTGTGT 771
```

RESULT 2
US-09-016-366A-20

Sequence 20, Application US/09016366A
Patent No. 595431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,366A

FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,090

FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7093

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1128 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-016-366A-20

Query Match 94.8%; Score 731; DB 2; Length 1128;
Best Local Similarity 98.7%; Pred. No. 1.1e-161;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
QY 17 GAATGTCGGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
DB 87 GCATGCTTGGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 146
QY 77 TCACGGCCCATATCTGATGCACTTCTGCGGGGCTCCCTCATACACCCCAAGTGGTGC 136
DB 147 TCACGGCCCATATCTGATGCACTTCTGCGGGGCTCCCTCATACACCCCAAGTGGTGC 206
QY 137 TGAACGCGCGCGCGTGTGAGACCGGACGTCAAGATCTGCGCGCTCAAGGTGCAAC 196
DB 207 TGAACGCGCGCGCGTGTGAGACCGGACGTCAAGATCTGCGCGCTCAAGGTGCAAC 266
QY 197 TGGGAGACAGACCTCTACTACAGACACAGCTGCTGCGGTGAGAGATCATGCTGC 256
DB 267 TGGGAGACAGACCTCTACTACAGACACAGCTGCTGCGGTGAGAGATCATGCTGC 326
QY 257 ACCCAAGTTTCAACCGCCCAAGATCGAGCGGACATGCGCTGCTGAGCTGAGAGAC 316
DB 327 ACCCAAGTTTCAACCGCCCAAGATCGAGCGGACATGCGCTGCTGAGCTGAGAGAC 386
QY 317 CGGTAAAGTCTCCAGCAAGTCCACAGGTCAACCTGCGCCCTGCTCAAGACCTTCC 376
DB 387 CGGTAAAGTCTCCAGCAAGTCCACAGGTCAACCTGCGCCCTGCTCAAGACCTTCC 446
QY 377 CCGCGGAGATGCGTGTGAGTCACTGCTGAGGCGATGAGACATGATGAGCGCTCC 436
DB 447 CCGCGGAGATGCGTGTGAGTCACTGCTGAGGCGATGAGACATGATGAGCGCGCTCC 506
QY 437 CACGCGCATTTCTCTGAGAGAGTGAAGTCCCATATGAGAAACCAATTGTGAGC 496
DB 507 CACGCGCATTTCTCTGAGAGAGTGAAGTCCCATATGAGAAACCAATTGTGAGC 566
QY 497 CAAATATCACTTGGCGCTTACACGGAGACAGTCCGATGCTCGGTACGACGATCG 556
DB 567 CAAATATCACTTGGCGCTTACACGGAGACAGTCCGATGCTCGGTACGACGATCG 626
```



```

/ FILING DATE: 05-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/7093
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1137 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/
US-09-016-366A-18

```

```

Query Match      94.8%; Score 731; DB 2; Length 1137;
Best Local Similarity 98.7%; Pred. No. 1,1e-161;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

/ 17 GATCGTCGGGGGTCAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
/ 85 GATCGTCGGGGGTCAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 144
/ 77 TCCACGGCCCATCTAGTGAATGCACTTCTGCGGGGCTCCCTCATCCACCCCAAGTGGTGC 136
/ 145 TCCACGGCCCATCTAGTGAATGCACTTCTGCGGGGCTCCCTCATCCACCCCAAGTGGTGC 204
/ 137 TGAACCCCGCGGCGTGGTGGGACCGGAGCTCAAGATCTGCGCCCTCAGGGTGAAC 196
/ 205 TGAACCCCGCGGCGTGGTGGGACCGGAGCTCAAGATCTGCGCCCTCAGGGTGAAC 264
/ 197 TGGGGAGGAGCAGCCTCTACTACAGAGCAGCTGCTGCGGGTCAAGAGATCATGTGC 256
/ 265 TGGGGAGGAGCAGCCTCTACTACAGAGCAGCTGCTGCGGGTCAAGAGATCATGTGC 324
/ 257 ACCCAGATTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGAGAGC 316
/ 325 ACCCAGATTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGAGAGC 384
/ 317 CGGTGAAGTCTTCAACGACGTCACACGGTCACTGCGCCCTGCTGAGAGCTTCC 376
/ 385 CGGTGAAGTCTTCAACGACGTCACACGGTCACTGCGCCCTGCTGAGAGCTTCC 444
/ 377 CCGGGGAGTGGCGTCTGGGTCAGTGGCTGGGGGAGTGGAGCAATGATGAGCGCTGC 436
/ 445 CCGGGGAGTGGCGTCTGGGTCAGTGGCTGGGGGAGTGGAGCAATGATGAGCGCTGC 504
/ 437 CACCGCATTTCTCTGAAGCAGGTGAAGTCCCATTAATGAAAAACAATTGTGAGC 496
/ 505 CACCGCATTTCTCTGAAGCAGGTGAAGTCCCATTAATGAAAAACAATTGTGAGC 564
/ 497 CAAAAATCACTTGGCGCTTACACGGGAGACGACGTCCGATCTGTCGTGAAGATGC 556
/ 565 CAAAAATCACTTGGCGCTTACACGGGAGACGACGTCCGATCTGTCGTGAAGATGC 624
/ 557 TGTGTCCCGGAAACACCGGAGGAGCTCATGACAGGGGACATCCGAGGGGCCCTGTGT 616
/ 625 TGTGTCCCGGAAACACCGGAGGAGCTCATGACAGGGGACATCCGAGGGGCCCTGTGT 684
/ 617 GCAAGGTGAATGGCATTGCTGACAGCGCGGCTGTGTCAGCTGGGGGAGAGGCTGTGCC 676
/ 685 GCAAGGTGAATGGCATTGCTGACAGCGCGGCTGTGTCAGCTGGGGGAGAGGCTGTGCC 744
/ 677 AGCCCAACCGGCTGGCATCTTACACCGGTCATCTTAATTGGACTGGAATCCAACT 736
/ 745 AGCCCAACCGGCTGGCATCTTACACCGGTCATCTTAATTGGACTGGAATCCAACT 804
/ 737 ATGTCCCAAAAAAGCGTGAAGCGGC 763
/ 805 ATGTCCCAAAAAAGCGTGAAGCGGC 831

```

```

RESULT 5
US-08-978-404B-13
/ Sequence 13, Application US/08978404B
/ Patent No. 5968782
/
/ GENERAL INFORMATION:
/ APPLICANT: Stevens, Richard L.
/ TITLE OF INVENTION: FAST CELL PROTEASE THAT CLEAVES
/ TITLE OF INVENTION: FIBRINOGEN
/ NUMBER OF SEQUENCES: 74
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02210-2211
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/978,404B
/
/ FILING DATE: 25-NOV-97
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/032,354
/
/ FILING DATE: 04-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/7090
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/
/
/
/
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1137 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-978-404B-13

```

```

Query Match      94.8%; Score 731; DB 2; Length 1137;
Best Local Similarity 98.7%; Pred. No. 1,1e-161;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

/ 17 GATCGTCGGGGGTCAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
/ 85 GATCGTCGGGGGTCAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 144
/ 77 TCCACGGCCCATCTAGTGAATGCACTTCTGCGGGGCTCCCTCATCCACCCCAAGTGGTGC 136
/ 145 TCCACGGCCCATCTAGTGAATGCACTTCTGCGGGGCTCCCTCATCCACCCCAAGTGGTGC 204
/ 137 TGAACCCCGCGGCGTGGTGGGACCGGAGCTCAAGATCTGCGCCCTCAGGGTGAAC 196
/ 205 TGAACCCCGCGGCGTGGTGGGACCGGAGCTCAAGATCTGCGCCCTCAGGGTGAAC 264
/ 197 TGGGGAGGAGCAGCCTCTACTACAGAGCAGCTGCTGCGGGTCAAGAGATCATGTGC 256
/ 265 TGGGGAGGAGCAGCCTCTACTACTACAGAGCAGCTGCTGCGGGTCAAGAGATCATGTGC 324
/ 257 ACCCAGATTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGAGAGC 316
/ 325 ACCCAGATTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGAGAGC 384
/ 317 CGGTGAAGTCTTCAACGACGTCACACGGTCACTGCGCCCTGCTGAGAGCTTCC 376
/ 385 CGGTGAAGTCTTCAACGACGTCACACGGTCACTGCGCCCTGCTGAGAGCTTCC 444

```


QY	CCCCGGGGAATGCCGTGTCAGGTCACCTGGGTGGGGGAGATGTGAAACAATGATGAGGCGCTCC	436
Db	445 CCCCCGGGGAATGCCGTGTCAGGTCACCTGGGTGGGGGAGATGTGAAACAATGATGAGGCGCTCC	504
QY	437 CACCGGCATTTTCCTCTGAAGACAGGTGAAGGTCCCATTAATGAAACCAACATTTGTGACG	496
Db	505 CACCGGCATTTTCCTCTGAAGACAGGTGAAGGTCCCATTAATGAAACCAACATTTGTGACG	564
QY	497 CAAAATATCAACTTTGGCGCTTACACGGGAGACGACGTCCGATGTCCGTGACGACATGC	556
Db	565 CAAAATATCAACTTTGGCGCTTACACGGGAGACGACGTCCGATGTCCGTGACGACATGC	624
QY	557 TGTGTCCTCCGGGACAACCCGGAGGGACTCATGCAAGGCGACTCCGGAGGGCCCTCGTGT	616
Db	625 TGTGTCCTCCGGGACAACCCGGAGGGACTCATGCAAGGCGACTCCGGAGGGCCCTCGTGT	684
QY	617 GCAAGGTGAATGGCACTTGCTGCAGGCGGGCGTGTGAGCTGGGGGCGAGGGCTGTGCC	676
Db	685 GCAAGGTGAATGGCACTTGCTGCAGGCGGGCGTGTGAGCTGGGGGCGAGGGCTGTGCC	744
QY	677 AGCCCAACGGGCTGGCATCTACACCCGTGTCACTTACTTGAACCTGATCCACACT	736
Db	745 AGCCCAACGGGCTGGCATCTACACCCGTGTCACTTACTTGAACCTGATCCACACT	804
QY	737 ATGTCCCAAAAAGCGGTGAAGCGGC	763
Db	805 ATGTCCCAAAAAGCGGTGAAGCGGC	831

RESULT 6

US-09-079-970A-1
; Sequence 1, Application US/09079970A
; Patent No. 6274366

GENERAL INFORMATION:
APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendelcho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property Department
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34506.073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2106
TELEFAX: (608) 831-2106
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

```

; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..735
;
US-09-079-970A-1

```

Query Match	94.5%	Score 728.6;	DB 3;	Length 735;
Best Local Similarity	99.5%;	Pred. No. 3.7e-161;		
Matches 731; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	19	ATCGTCGGGGGTCAAGAGAGCGCCAGAGAGCAAGTGCCCTGGCAGGTGAGCCTGAGACTC	78
Db	1	ATCGTCGGGGGTCAAGAGAGCGCCAGAGAGCAAGTGCCCTGGCAGGTGAGCCTGAGACTC	60
QY	79	CACGGCCCATACCTGGATGACCTTCTGCGGGGGCTCCTCATTCACCCCAAGTGGGTCTG	138
Db	61	CACGGCCCATACCTGGATGACCTTCTGCGGGGGCTCCTCATTCACCCCAAGTGGGTCTG	120
QY	139	ACCGCCGGCGCGTGGCGGTGGGACCCGAGCGTCAGAGGATCTGGCCGCGCTTCAGGGTGCAC	198
Db	121	ACCGCACCGACCTGGCGGTGGGACCCGAGCGTCAGAGGATCTGGCCGCGCTTCAGGGTGCAC	180
QY	199	CGGAGAGAGCAGCTCTACTACCAAGACCAAGCTGTCGCGGTCAAGAGATCATCGTGAC	258
Db	181	CGGAGAGCAGACCTCTACTACCAAGACCAAGCTGTCGCGGTCAAGAGATCATCGTGAC	240
QY	259	CCACAGTTTCAACACCGCCAGATCGAGCGGACATCGCCCTGCTGGAGCTGAGAGCGG	318
Db	241	CCACAGTTTCAACACCGCCAGATCGAGCGGACATCGCCCTGCTGGAGCTGAGAGAGCGG	300
QY	319	GTGAAGGTCTTCAGACCAAGTCACACAGGTACCTTGCCCTGGCTCAGAACTTTCCCC	378
Db	301	GTGAAGGTCTTCAGACCAAGTCACACAGGTACCTTGCCCTGGCTCAGAACTTTCCCC	360
QY	379	CCGGGGAGTGCAGTCTGGGTCACTGCGCTGGGGCGATGTGGAACAATGATAGAGCGCTCCCA	438
Db	361	CCGGGGAGTGCAGTCTGGGTCACTGCGCTGGGGCGATGTGGAACAATGATAGAGCGCTCCCA	420
QY	439	CCGCCATTTCCTCTGGAAGCAGGTGAAGGTCCCATTAATGAAAAACCACTTTGTGACGCA	498
Db	421	CCGCCATTTCCTCTGGAAGCAGGTGAAGGTCCCATTAATGAAAAACCACTTTGTGACGCA	480
QY	499	AAATACCACTTTGGCGCTTACACGGGAGACGACGTCCGACATGTCCTGTGACGACATGCTG	558
Db	481	AAATACCACTTTGGCGCTTACACGGGAGACGACGTCCGACATGTCCTGTGACGACATGCTG	540
QY	559	TGTGCGCGGGAAACACCGCGAGGGACTCAATGCCAGGGGCGACTCCGAGGGGCCCTGGTGTGC	618
Db	541	TGTGCGCGGGAAACACCGCGAGGGACTCAATGCCAGGGGCGACTCCGAGGGGCCCTGGTGTGC	600
QY	619	AAGGTGAATGGACCTTGAGTCGACGAGCGGCGCTGGTCAAGCTGGAGGAGCTGTGCCAG	678
Db	601	AAGGTGAATGGACCTTGAGTCGACGAGCGGCGCTGGTCAAGCTGGAGGAGCTGTGCCAG	660
QY	679	CCCAACCGGCGCTGGCATCTTACACCGGTGTCACTTACTTGGATCTGATTCACCATAT	738
Db	661	CCCAACCGGCGCTGGCATCTTACACCGGTGTCACTTACTTGGATCTGATTCACCATAT	720
QY	739	GTCCGCCAAAAACCG 753	
Db	721	GTCCGCCAAAAACCG 735	

RESULT 7

US-09-016-366A-22
Sequence 22, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
INVENTOR: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS

```

1 NUMBER OF SEQUENCES: 65
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
4 STREET: 600 Atlantic Avenue
5 CITY: Boston
6 STATE: MA
7 COUNTRY: U.S.A.
8 ZIP: 02210-2211
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Diskette
11 COMPUTER: IBM Compatible
12 OPERATING SYSTEM: DOS
13 SOFTWARE: FastSeq for Windows Version 2.0
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09/016,366A
16 FILING DATE: January 30, 1998
17 CLASSIFICATION: 530
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 60/037,090
20 FILING DATE: 05-FEB-1997
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Plummer, Elizabeth R.
23 REGISTRATION NUMBER: 36,637
24 REFERENCE/DOCKET NUMBER: B0801/7093
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 617-720-3500
27 TELEFAX: 617-720-2441
28
29
30 INFORMATION FOR SEQ ID NO: 22:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 1081 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36
37 MOLECULE TYPE: CDNA
38
39 US-09-016-366A-22

```

Query Match	Similarity	94.2%	Score 726.2	DB 2	Length 1081
Best Local	Similarity	98.3%	Pred. No. 1.5e-160		
Matches	734	Conservative	0	Mismatches 13	Indels 0
				Gaps	0
QY	17	GAATGTCGGGGGCTGAGAGGCCCCCAGAGAGCAAGTGGCCCTGCGAGTGAACCTTGAGAG	76		
Db	66	GCATCGTTGGGGGCTGAGAGGCCCCCAGAGAGCAAGTGGCCCTGCGAGTGAACCTTGAGAG	125		
QY	77	TCGACGGCCATPACTGAGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCAATGGGGTGC	136		
Db	126	TCCGCGACCGATCTGAGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCAATGGGGTGC	185		
QY	137	TGACCGCGCGGGCGTGCCTGGAGCCGGAAGTCAAGAGATCTGGCCGCCCTCAGGGTGAAC	196		
Db	186	TGACCGCGCGGCACCTGCGTGGGACCGGAGCGTCAAGAGATCTGGCCGCCCTCAGGGTGAAC	245		
QY	197	TGCGGGACACAGCACTCTACTACCAAGGACCAAGCTCTGCGCGTCAAGAGATCATCGTGC	256		
Db	246	TGCGGGACAGCACTCTACTACCAAGGACCAAGCTCTGCGCGTCAAGAGATCATCGTGC	305		
QY	257	ACCACAGTTCTACACCGGCCAGATCGAGCGGAGATGCGCTGCTGAGGTGAGAGAC	316		
Db	306	ACCACAGTTCTACACCGGCCAGATCGAGCGGAGATGCGCTGCTGAGGTGAGAGAC	365		
QY	317	CGGTGAAGTCTTCAGCCACGCTCCACAGGTCAACCTTGCCCTTCACAGACTTTC	376		
Db	366	CGGTGAAGTCTTCAGCCACGCTCCACAGGTCAACCTTGCCCTTCACAGACTTTC	425		
QY	377	CCCCGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACATATGAGCGCCTCC	436		
Db	426	CCCCGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACATATGAGCGCCTCC	485		
QY	437	CACGCGCATTTCTCTGAGACAGGTGAAGGTCCCATATGAGAAACCACTATTGTGAC	496		
Db	486	CACGCGCATTTCTCTGAGACAGGTGAAGGTCCCATATGAGAAACCACTATTGTGAC	545		

[illegible]

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

QY 77 TCACAGGCGCCATCTGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 136
DB 126 TCCGGAACCGGATCTGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 185
QY 137 TGAACCGCGCGCGCTGCTGGGACCGGACGTCAGAGATCTGAGCGCCCTCAGGGTGCAC 196
DB 186 TGACCGGACGCGACGCTGGGACCGGACGTCAGAGATCTGAGCGCCCTCAGGGTGCAC 245
QY 197 TGGGGAGACGACCTCTACTACAGGACGAGCTGCTGCGGCTCGAGGAGATCATCTGTC 256
DB 246 TGGGGAGACGACCTCTACTACAGGACGAGCTGCTGCGGCTCGAGGAGATCATCTGTC 305
QY 257 ACCCAGATTCTACACCGCCGAGTCGAGCGGACATGCGCTGTGAGCTGAGAGAC 316
DB 306 ACCCAGATTCTACACCGCCGAGTCGAGCGGACATGCGCTGTGAGCTGAGAGAC 365
QY 317 CGGTGAAGGTCTCAAGCGACGTCACACGCTGACCCCTGCTCGAGAGACTTTC 376
DB 366 CGGTGAAGGTCTCAAGCGACGTCACACGCTGACCCCTGCTCGAGAGACTTTC 425
QY 377 CCCCAGGAGATGCGCTGCTGGTCACTGCTGGGCGAGATGAGACATATGATGAGCGCTTC 436
DB 426 CCCCAGGAGATGCGCTGCTGGTCACTGCTGGGCGAGATGAGACATATGATGAGCGCTTC 485
QY 437 CACCGCATTTCTCTGAGAGAGTGAAGGTCCCATATGAGAAACACATTTGTGACG 496
DB 486 CACCGCATTTCTCTGAGAGAGTGAAGGTCCCATATGAGAAACACATTTGTGACG 545
QY 497 CAAAATACACCTTGGCGCTTACACGAGGAGACGATCGTCGCTGCTGAGACATGC 556
DB 546 CAAAATACACCTTGGCGCTTACACGAGGAGACGATCGTCGCTGCTGAGACATGC 605
QY 557 TGTGTGCGGGGAAACCGGAGAGACTCATGCTCAGGAGGAGCTCCGAGAGGCGCTGTGT 616
DB 606 TGTGTGCGGGGAAACCGGAGAGACTCATGCTCAGGAGGAGCTCCGAGAGGCGCTGTGT 665
QY 617 GCAAGGTGAATGGACCTGCTGACGAGCGGCGCTGCTGACGCTGAGGCGGCTGTGCTC 676
DB 666 GCAAGGTGAATGGACCTGCTGACGAGCGGCGCTGCTGACGCTGAGGCGGCTGTGCTC 725
QY 677 AGCCCAACCGGCTGCGCATCTACACCCGCTGCTACCTACTTGGACTGTATCCACACT 736
DB 726 AGCCCAACCGGCTGCGCATCTACACCCGCTGCTACCTACTTGGACTGTATCCACACT 785
QY 737 ATGTCCCCCAAAAAGCGTGAAGCGGCC 763
DB 786 ATGTCCCCCAAAAAGCGTGAAGCGGCC 812

RESULT 9
US-09-917-254-50
; Sequence 50, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224 (RV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-917-254-50

Query Match 94.2%; Score 726.2; DB 4; Length 1081;
Best Local Similarity 98.3%; Pred. No. 1.5e-160;
Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 GAATGCTGGGGGTCAGAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
DB 66 GCATGTTGGGGGTCAGAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 125
QY 77 TCACAGGCGCCATCTGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 136
DB 126 TCCGGAACCGGATCTGATGACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 185
QY 137 TGAACCGCGCGCGCTGCTGGGACCGGACGTCAGAGATCTGAGCGCCCTCAGGGTGCAC 196
DB 186 TGACCGGACGCGACGCTGGGACCGGACGTCAGAGATCTGAGCGCCCTCAGGGTGCAC 245
QY 197 TGGGGAGACGACCTCTACTACAGGACGAGCTGCTGCGGCTCGAGGAGATCATCTGTC 256
DB 246 TGGGGAGACGACCTCTACTACAGGACGAGCTGCTGCGGCTCGAGGAGATCATCTGTC 305
QY 257 ACCCAGATTCTACACCGCCGAGTCGAGCGGACATGCGCTGTGAGCTGAGAGAC 316
DB 306 ACCCAGATTCTACACCGCCGAGTCGAGCGGACATGCGCTGTGAGCTGAGAGAC 365
QY 317 CGGTGAAGGTCTCAAGCGACGTCACACGCTGACCCCTGCTCGAGAGACTTTC 376
DB 366 CGGTGAAGGTCTCAAGCGACGTCACACGCTGACCCCTGCTCGAGAGACTTTC 425
QY 377 CCCCAGGAGATGCGCTGCTGGTCACTGCTGGGCGAGTGGACATATGATGAGCGCTTC 436
DB 426 CCCCAGGAGATGCGCTGCTGGTCACTGCTGGGCGAGTGGACATATGATGAGCGCTTC 485
QY 437 CACCGCATTTCTCTGAGAGAGTGAAGGTCCCATATGAGAAACACATTTGTGACG 496
DB 486 CACCGCATTTCTCTGAGAGAGTGAAGGTCCCATATGAGAAACACATTTGTGACG 545
QY 497 CAAAATACACCTTGGCGCTTACACGAGGAGACGATCGTCGCTGCTGAGACATGC 556
DB 546 CAAAATACACCTTGGCGCTTACACGAGGAGACGATCGTCGCTGCTGAGACATGC 605
QY 557 TGTGTGCGGGGAAACCGGAGAGACTCATGCTCAGGAGGAGCTCCGAGAGGCGCTGTGT 616
DB 606 TGTGTGCGGGGAAACCGGAGAGACTCATGCTCAGGAGGAGCTCCGAGAGGCGCTGTGT 665
QY 617 GCAAGGTGAATGGACCTGCTGACGAGCGGCGCTGCTGACGCTGAGGCGGCTGTGCTC 676
DB 666 GCAAGGTGAATGGACCTGCTGACGAGCGGCGCTGCTGACGCTGAGGCGGCTGTGCTC 725
QY 677 AGCCCAACCGGCTGCGCATCTACACCCGCTGCTACCTACTTGGACTGTATCCACACT 736
DB 726 AGCCCAACCGGCTGCGCATCTACACCCGCTGCTACCTACTTGGACTGTATCCACACT 785
QY 737 ATGTCCCCCAAAAAGCGTGAAGCGGCC 763
DB 786 ATGTCCCCCAAAAAGCGTGAAGCGGCC 812

RESULT 10
US-09-016-366A-16
; Sequence 16, Application US/09016366A
; Patent No. 5953431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P. C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-16

```

```

Query Match      89.0%; Score 686.2; DB 2; Length 1154;
Best Local Similarity 94.3%; Pred. No. 3.3e-151;
Matches 712; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```

```

QY 17 GAATGCTGGGGGTCAAGAGCGCCCGAGAGCAAGTGGCCCTGCGAGTGAAGCTTAGAG 76
DB 106 GTATGCTGGGGGTCAAGAGCGCCCGAGAGCAAGTGGCCCTGCGAGTGAAGCTTAGAG 165
QY 77 TCACGGGCCCATCTGGATGACCTTCTGCGGGGGCTCCCTCATCCAGCCCAATGGGTGC 136
DB 166 TCCGCAACCATATCTGATGACCTTCTGCGGGGGCTCCCTCATCCAGCCCAATGGGTGC 225
QY 137 TGACCGCGCGCGGTGCTGGGAGCCGAGCACTCAAGGATCTGCGCGCCCTCAGGGTCAAC 196
DB 226 TGACCGCGCGCGGTGCTGGGAGCCGAGCACTCAAGGATCTGCGCGCCCTCAGGGTCAAC 285
QY 197 TGGGGAGAGCACTCTACTACCAAGACCAAGTGTCTCCGGGTCAAGAGATCATGTGC 256
DB 286 TGGGGAGAGCACTCTACTACCAAGACCAAGTGTCTCCGGGTCAAGAGATCATGTGC 345
QY 257 ACCCAGATTCTACACCGCCAGATGAGCGGAGCAGTCCGCTGAGCTGAGAGTGAAGC 316
DB 346 ACCCAGATTCTACACCGCCAGATGAGCGGAGCAGTCCGCTGAGCTGAGAGTGAAGC 405
QY 317 CGGTGAAGTCTCTCAGCAGTCCAGACGCTCACTGCGCCCTGCTGAGAGCTTCC 376
DB 406 CGGTGAAGTCTCTCAGCAGTCCAGACGCTCACTGCGCCCTGCTGAGAGCTTCC 465
QY 377 CCCCCGAGTGGCTGCTGGTCACTGGTGGGCGCATGTGCAATGATGAGCGCTTC 436
DB 466 CCCCCGAGTGGCTGCTGGTCACTGGTGGGCGCATGTGCAATGATGAGCGCTTC 525
QY 437 CACCGCATTTCTCTGAGAGCAGTGAAGGTCCCAATATGAAAAACAATTGTTGAG 496
DB 526 CACCGCATTTCTCTGAGAGCAGTGAAGGTCCCAATATGAAAAACAATTGTTGAG 585
QY 497 CAAATATACACCTTGGCGCTACACGAGAGACAGACGTCCGATCTCGTGAAGCATGC 556
DB 586 CAAATATACACCTTGGCGCTACACGAGAGAGACAGACGTCCGATCTCGTGAAGCATGC 645
QY 557 TGTGTCCGAGAAACACCCGAGAGGACTCATGCCAGGCGCATCTCCGAGAGGCCCTGTGT 616
DB 646 TGTGTCCGAGAAACACCCGAGAGGACTCATGCCAGGCGCATCTCTGAGAGGCCCTGTGT 705
QY 617 GCAGAGTGAATGACCTGCTGACGAGCGGGGCTGCTGAGCTGAGAGGCGTGTGCC 676

```

```

DB 706 GCAGAGTGAATGACCTGCTGACAGCGGGGCTGTGACGTGGAGACAGAGGCTGTGCC 765
QY 677 AGCCCAACCGGCGTGGCATCTACACCGGCTGACCTGACTTGGACTGATCCAGACT 736
DB 766 AGCCCAACCGGCGTGGCATCTACACCGGCTGATCCACTTACTTGAATGATCCAGACT 825
QY 737 ATGTCCCAAAAAAGCGTGAAGCGGCGCGCTGCT 771
DB 826 ATGTCCCAAAAAAGCGTGAAGCGGCGCTGCTGCT 860

```

```

RESULT 11
US-08-978-404B-11
Sequence 11, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
NUMBER OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-11

```

```

Query Match      89.0%; Score 686.2; DB 2; Length 1154;
Best Local Similarity 94.3%; Pred. No. 3.3e-151;
Matches 712; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```

```

QY 17 GAATGCTGGGGGTCAAGAGCGCCCGAGAGCAAGTGGCCCTGCGAGTGAAGCTTAGAG 76
DB 106 GTATGCTGGGGGTCAAGAGCGCCCGAGAGCAAGTGGCCCTGCGAGTGAAGCTTAGAG 165
QY 77 TCACGGGCCCATCTGATGACCTTCTGCGGGGGCTCCCTCATCCAGCCCAATGGGTGC 136
DB 166 TCCGCAACCATATCTGATGACCTTCTGCGGGGGCTCCCTCATCCAGCCCAATGGGTGC 225
QY 137 TGACCGCGCGCGGTGCTGGGAGCCGAGCACTCAAGGATCTGCGCGCCCTCAGGGTCAAC 196
DB 226 TGACCGCGCGCGGTGCTGGGAGCCGAGCACTCAAGGATCTGCGCACCTCAGGGTCAAC 285
QY 197 TGGGGAGAGCACTCTACTACCAAGACCAAGTGTCTCCGGGTCAAGAGATCATGTGC 256

```


Db	766	CACAGCCCAACAGGCTGCGATCTACACCGGGTCACTATTACTTGACTGGATCCACC	825
Qy	734	ACTATGTCCCCCAAAAAGCGGTGA	756
Db	826	ACTATGTCCCCCAAGACTTCTGA	848

Search completed: August 27, 2005, 19:37:45
Job time : 191 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2005, 23:19:35 ; Search time 56 Seconds
(without alignments)
472.493 Million cell updates/sec

Title: US-09-598-982C-52

Perfect score: 1512
Sequence: 1 MSLTLLALPVLASRAVAAP.....ITRTVTVYLDWIMHHVPRKP 275

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1470.5	97.3	274	2	A45754
2	1430	94.6	275	2	C35863
3	1411	93.3	275	2	A35863
4	1405	92.9	275	2	B35863
5	1134	75.0	273	2	A47246
6	1133	74.9	276	2	A38654
7	1131	74.8	275	2	A32410
8	1109.5	73.4	270	2	S56160
9	1105	73.1	274	2	JC4171
10	999	66.1	237	2	S68702
11	856	56.6	230	2	I48685
12	686.5	45.4	269	2	B32410
13	516	34.1	343	1	A57014
14	468	31.0	625	1	KFH01
15	465	30.8	638	1	KOHUP
16	461	30.5	638	1	KOHUP
17	459.5	30.4	271	1	ELRT2
18	457.5	30.3	245	1	KYBOB
19	454	30.0	455	2	A61545
20	454	30.0	638	1	KORPL
21	451.5	29.9	812	1	PLBO
22	448	29.6	460	2	B61545
23	447.5	29.6	269	2	B26823
24	440.5	29.1	263	2	A31299
25	439	29.0	810	1	PLHU
26	438.5	29.0	263	2	A21195
27	438.5	29.0	271	2	A25528
28	434	28.7	263	1	KYRTB
29	434	28.7	810	2	B30848

30	429.5	28.4	4548	1	S00657	apoptein(a) (EC
31	429	28.4	266	1	ELPG	pancreatic elastase
32	429	28.4	1524	2	T30337	polypeptide - Afri
33	428.5	28.3	367	2	JB0104	testicular serine
34	426.5	28.2	269	2	C26823	pancreatic elastase
35	425.5	28.1	812	1	PLMS	plasma (EC 3.4.21
36	425	28.1	245	1	KYBOA	chymotrypsin (EC 3
37	425	28.1	790	1	PLPG	trypsin (EC 3.4.21
38	424	28.0	246	2	B25528	acrosin (EC 3.4.21
39	423.5	28.0	436	2	UX0172	acrosin (EC 3.4.21
40	421.5	27.9	810	2	I46260	plasma (EC 3.4.21
41	420.5	27.8	263	2	S47537	chymotrypsin (EC 3
42	417.5	27.6	270	2	A29934	pancreatic elastase
43	417	27.6	264	2	I38136	chymotrypsin-like
44	415	27.4	421	2	S29599	acrosin (EC 3.4.21
45	414	27.4	786	1	A47547	serine proteinase

ALIGNMENTS

RESULT 1
A45754
trypsin (EC 3.4.21.59) alpha precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
C:Accession: A45754; B37193
R:Miller, J.S.; Westin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1989
A:Title: Cloning and characterization of complementary DNA for human trypsin.
A:Reference number: A45754; MUID:90009311; PMID:2677049
A:Accession: A45754
A:Molecule type: mRNA
A:Residues: 1-274 <MT>
A:Cross-references: GB:M30038
R:Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A:Title: Cloning and characterization of a second complementary DNA for human trypsin.
A:Reference number: A37193; MUID:90369005; PMID:2203827
A:Accession: B37193
A:Molecule type: mRNA
A:Residues: 1-274 <MT>
A:Cross-references: GB:M30038
A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-Pro
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-30/Domain: activation peptide #status predicted <ACT>
F:31-274/Product: trypsin I #status predicted <MAT>
F:31-266/Domain: trypsin homology <TRY>
F:74,120,223/Active site: His, Asp, Ser #status predicted

Query Match	97.3%	Score 1470.5;	DB 2;	Length 274;
Best Local Similarity	97.8%	Pred. No. 3.56-123;		
Matches 269;	Conservative 1;	Mismatches 4;	Indels 1;	Gaps 1;
QY	1	MSLTLLALPVLASRAVAAPVQALQAGIVGQEARSKMPQVSRVDRYMHPCG	60	
DB	1	MSLTLLALPVLASRAVAAPVQALQAGIVGQEARSKMPQVSRVDRYMHPCG	60	
QY	61	GSLLHPQVLTFRACLGPDVDTLTRYQLEOHLYYQDQLPVSRILVHPQFIITGGA	120	
DB	61	GSLLHPQVLTFRACLGPDVDTLTRYQLEOHLYYQDQLPVSRILVHPQFIITGGA	119	
QY	121	DIALLEEPVNISRVTWLPASSETPPGMCWVTGWGVNDDEPLPPFPKQYKV	180	
DB	120	DIALLEEPVNISRVTWLPASSETPPGMCWVTGWGVNDDEPLPPFPKQYKV	179	
QY	181	PIMENHICDACYHGGATYGDVRIIRDDMLCAGNSQSDSCGSDGGLVCKVNGTWLQAG	240	
DB	180	PIMENHICDACYHGGATYGDVRIIRDDMLCAGNSQSDSCGSDGGLVCKVNGTWLQAG	239	
QY	241	VVSNDEGCAQPNRPGIYRTVTVYLDWIMHHVPRKP	275	

Db 240 VVSMDEGCAQPNRPGIYTRVTYLLDWIHVYPKP 274

RESULT 2

tryptase (EC 3.4.21.59) III precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 07-Mar-2003
 C:Accession: C35863; E35863; A38893
 R:Vanderelice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
 A:Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
 A:Reference number: A35863; MUID:90251647; PMID:2187193
 A:Accession: C35863
 A:Molecule type: mRNA
 A:Residues: 9-275 <VAN>
 A:Accession: E35863
 A:Molecule type: DNA
 A:Residues: 1-9 <VA2>
 A:Cross-references: GB:M33494; NID:G3927804; PIDN:AA083172.1; PID:G339977
 A:Note: the first nine residues of this sequence are inferred from genomic DNA of trypt
 R:Vanderelice, P.
 Submitted to GenBank, April 1990
 A:Reference number: A38893
 A:Accession: A38893
 A:Molecule type: mRNA
 A:Residues: 9-131, 'K', 132-275 <VA3>
 A:Cross-references: GB:M33493; NID:G339984; PIDN:AAA6780.1; PID:G339985
 C:Superfamily: trypsin, trypsin homology
 C:Keywords: hydrolase; serine proteinase; zymogen
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-30/Domain: activation peptide #status predicted <ACT>
 F:31-275/Product: trypsin I #status predicted <MAT>
 F:31-267/Domain: trypsin homology <TRY>
 F:74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 94.6%; Score 1430; DB 2; Length 275;
 Best Local Similarity 93.5%; Pred. No. 1.4e-119;
 Matches 257; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSLLLALPVLASRAVAAPAVQALQAGIVGGGEAPRSKMPQVSLVRDRYMHFCG 60
 DB 1 MNLILLALPVLASRAVAAPAVQALQAGIVGGGEAPRSKMPQVSLVRDRYMHFCG 60
 QY 61 GSLIHQWVLTAAHCGPVDKDLALRVQLRBOHLYYDOLLPVSRITVHPOFYTAQTGA 120
 DB 61 GSLIHQWVLTAAHCGPVDKDLALRVQLRBOHLYYDOLLPVSRITVHPOFYTAQTGA 120
 QY 121 DIALLELEBPVNISRHVTVMLEPPASETFPPGMPGVTGMDVNDDEPLPPFPPLKQYKV 180
 DB 121 DIALLELEBPVNISRHVTVMLEPPASETFPPGMPGVTGMDVNDDEPLPPFPPLKQYKV 180
 QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNSORDSCKDGSGGPLVCKVNGTWLQAG 240
 DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNSORDSCKDGSGGPLVCKVNGTWLQAG 240
 QY 241 VVSMDEGCAQPNRPGIYTRVTYLLDWIHVYPKP 275
 DB 241 VVSMDEGCAQPNRPGIYTRVTYLLDWIHVYPKP 275

RESULT 3

tryptase (EC 3.4.21.59) I precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 12-Oct-1990 #sequence revision 12-Oct-1990 #text_change 09-Jul-2004
 C:Accession: A35863; D35863; A60939; A39326
 R:Vanderelice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
 A:Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
 A:Reference number: A35863; MUID:90251647; PMID:2187193
 A:Accession: A35863

A:Molecule type: DNA
 A:Residues: 1-275 <VAN>
 A:Cross-references: UNIPROT:Q15661; GB:M33494; NID:G3927804; PIDN:AA083172.1; PID:G339977
 A:Accession: D35863
 A:Molecule type: mRNA
 A:Residues: 1-275 <VA2>
 A:Cross-references: GB:M33491
 R:Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, P.C. J. Leukoc. Biol. 47, 409-419, 1990
 A:Title: Purification of tryptase from a human mast cell line.
 A:Reference number: A60939; MUID:90244210; PMID:2110591
 A:Accession: A60939
 A:Molecule type: protein
 A:Residues: 31-38, 'P', 40-41, 'X', 43, 'T', 45-48, 'X', 50 <BUT>
 A:Experimental source: mast cell
 A:Note: 44-Gly was also found
 R:Cromlish, J.A.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Johnson, D.A.; Chretien, U. Biol. Chem. 262, 1363-1373, 1987
 A:Title: Human pituitary tryptase: molecular forms, NH-2-terminal sequence, immunocytoche
 A:Reference number: A39326; MUID:87109258; PMID:3543004
 A:Accession: A39326
 A:Molecule type: protein
 A:Residues: 31-38 <CRO>
 A:Experimental source: pituitary
 C:Genetics:
 A:introns: 21/1; 78/2; 177/1; 221/3
 C:Superfamily: trypsin, trypsin homology
 C:Keywords: hydrolase; serine proteinase; zymogen
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-30/Domain: activation peptide #status predicted <ACT>
 F:31-275/Product: trypsin I #status experimental <MAT>
 F:31-267/Domain: trypsin homology <TRY>
 F:74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 93.3%; Score 1411; DB 2; Length 275;
 Best Local Similarity 92.4%; Pred. No. 6.8e-118;
 Matches 254; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSLLLALPVLASRAVAAPAVQALQAGIVGGGEAPRSKMPQVSLVRDRYMHFCG 60
 DB 1 MNLILLALPVLASRAVAAPAVQALQAGIVGGGEAPRSKMPQVSLVRDRYMHFCG 60
 QY 61 GSLIHQWVLTAAHCGPVDKDLALRVQLRBOHLYYDOLLPVSRITVHPOFYTAQTGA 120
 DB 61 GSLIHQWVLTAAHCGPVDKDLALRVQLRBOHLYYDOLLPVSRITVHPOFYTAQTGA 120
 QY 121 DIALLELEBPVNISRHVTVMLEPPASETFPPGMPGVTGMDVNDDEPLPPFPPLKQYKV 180
 DB 121 DIALLELEBPVNISRHVTVMLEPPASETFPPGMPGVTGMDVNDDEPLPPFPPLKQYKV 180
 QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNSORDSCKDGSGGPLVCKVNGTWLQAG 240
 DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNSORDSCKDGSGGPLVCKVNGTWLQAG 240
 QY 241 VVSMDEGCAQPNRPGIYTRVTYLLDWIHVYPKP 275
 DB 241 VVSMDEGCAQPNRPGIYTRVTYLLDWIHVYPKP 275

RESULT 4

tryptase (EC 3.4.21.59) II precursor - human
 N:Alternate names: tryptase beta
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: B35863; A37193; T59473
 R:Vanderelice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
 A:Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
 A:Reference number: A35863; MUID:90251647; PMID:2187193
 A:Accession: B35863
 A:Molecule type: mRNA
 A:Residues: 1-275 <VAN>

C:Superfamily: trypsin; trypsin homology	
C:Keywords: hydrolase; serine proteinase	
P:29-265/Domain: trypsin homology <TRY>	
Query Match	75.0%; Score 1134; DB 2; Length 273;
Best Local Similarity	74.4%; Pred. No. 2, 8e-93;
Matches 203; Conservative	23; Mismatches 45; Indels 2; Gaps 1;
QY	1 M L S L I L L L P V L A S R A Y A P A R V Q A L Q A G I Y G G E A R P S K M Q V S L A R D R T W M H F C G 60
DB	1 M K L I L L T L P L I L S L V H A A G P - A A M T R E G I Y G G E A H G K M Q V S L R A N D I T W M H F C G 58
QY	61 G S L I H P W V L T F A A H C I G P D V K D L A T L R V Q L R E Q H L Y Y O D L L P V S R I I V H P Q F Y I I T G A 120
DB	59 G S L I H P W V L T F A A H C V G P V A D P N K V R V Q L R K Q L Y L Y H D H L M T V S Q I I T H P D F I T V D G A 118
QY	121 D I A L L E L E B P V N I S S R V H T V M L P P A S E T P P P G M F C W T G K G V D V N D E P L P P P F L K O V Y 180
DB	119 D I A L L K T I N P V N I S D V H P V L P P P A S E T P P S G T L C W T G N I D N G V N L P P P F L K E V Q V 178
QY	181 P L M E N H I C D A K A H L G A Y T G D V R I I R I D D M L C A G N S O R D S C K G P S G G F L V C K V N G T W L Q A G 240
DB	179 P L I E N H L C D L K A H K G L I T G D V N H I V R D D M L C A G N E G H D S C G S D S G G F L V C K V E D T W L Q A G 238
QY	241 V V S M D E G C A Q P N R P G I Y T R V T Y Y L D M I H H Y V P K 273
DB	239 V V S M G E G C A Q P N R P G I Y T R V T Y Y L D M I H H Y V P K 271

C:Species: Mus musculus (house mouse)
C.Date: 21-Feb-1992 #sequence revision 17-Feb-1994 #text_change 09-Jul-2004
C.Accession: A38654; B38654; D35646; I59478
R.Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
U. Biol. Chem. 266, 3847-3853, 1991
A.Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by pro-
A.Reference number: A38654; MUID:91139682; PMID:1995638
A.Molecule type: mRNA
A.Residues: 1-276 <REV>
A.Cross-references: UNIPROT:P21845; GB:M57625; NID:g200506; PID:AAA3987.1; PID:g200507
A.Note: the authors transcribed the codon CGC for residue 24 as Ala, GAG for residue 37 as
s Gly. GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
A.Accession: B38654
A.Molecule type: mRNA
A.Residues: 1-276 <REV>
A.Cross-references: GB:M57626; NID:g200508; PID:AAA3988.1; PID:g200509
R.Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A.Title: Different mouse mast cell populations express various combinations of at least
A.Reference number: A35646; MUID:90222202; PMID:236280
A.Accession: D35646
A.Molecule type: protein
A.Residues: 32-54 <RE3>
R.Huang, R.; Abbrink, M.; Gohl, A.E.; Nilsson, G.; Aveskog, M.; Larsson, L.G.; Nilsson, L.
Scand. J. Immunol. 38, 359-367, 1993
A.Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and
A.Reference number: I59478; MUID:94023807; PMID:8210958
A.Accession: I59478
A.Molecule type: mRNA
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Residues: 1-276 <RES>
A.Cross-references: GB:LJ1853; NID:g473480; PID:AAA39725.1; PID:g473481
C.Genetics:
A.Gene: MMCP-6
A.Introns: 24/1; 79/2; 168/1; 222/3
C.Superfamily: trypsin; trypsin homology
C.Keywords: hydrolase; serine proteinase; zymogen
F.1-21/Domain: signal sequence #status predicted <SIG>
F.22-31/Domain: activation peptide #status predicted <ACT>
F.32-376/Product: mast cell proteinase 6 #status experimental <MAT>

F;32-268/Domain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser #status predicted

Query Match 74.9%; Score 1133; DB 2; Length 276;
Best Local Similarity 73.3%; Pred. No. 3, 5e-93;
Matches 198; Conservative 28; Mismatches 42; Indels 2; Gaps 1;

QY 4 LLLALLPVLASRAVAPAVQALQAGIVGGGEAPRSKMPQVSLRDRYMMHFCGSL 63
DB LLLMALSLASLAVYSAPRP--ANQGVIGVGHSEASKEKMPQVSLRFLKNTYIHFPGSL 64
QY 64 IHQWVLTAAHCLGPRVQKDLATLRVQLRBNLYYQOQLPVSIIYHPQFYIIQTGADTA 123
DB 65 IHQWVLTAAHCLGPRVQKDLATLRVQLRBNLYYQOQLPVSIIYHPQFYIIQTGADTA 124
QY 124 LLELEBPVNISSRVHTVTLPPASETFPPGMPGCVTWGMDVNDDEPLPPFPPLKQVAV 183
DB 125 LLELEBPVNISSRVHTVTLPPASETFPPGMPGCVTWGMDVNDDEPLPPFPPLKQVAV 184
QY 184 ENHICDAKXHLGAYTGDVRIIRDMLCAGNSQSDSCKDSGGPLVCYKNGTWLQAGVVS 243
DB 185 ENSLCDRKXHTGLYTGDDEPLVHDMGLCAGNTRRSDSCGDSGGPLVCYKNGTWLQAGVVS 244
QY 244 WDEGCAQPNRPGIYTRVTVYLLDMIHRYVPE 273
DB 245 WDEGCAQPNRPGIYTRVTVYLLDMIHRYVPE 274

RESULT 7

A32410
trypsin (EC 3.4.21.59) precursor - dog
C/Species: Canis lupus familiaris (dog)
C/Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jul-2004
C/Accession: A32410
R/Vanderlisse, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4148-4155, 1989
A/Title: Molecular cloning of dog mast cell tryptase and a related protease: structural
A/Reference number: A32410; MUID:89352460; PMID:2504277
A/Accession: A32410
A/Molecule type: rRNA
A/Residues: 1-275 <VAN>
A/Cross-references: UNIPROT:P15944; GB:M24664; NID:g163982; PIND:AAA30854.1; PID:g163983
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase #status predicted <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 74.8%; Score 1131; DB 2; Length 275;
Best Local Similarity 72.7%; Pred. No. 5, 3e-93;
Matches 200; Conservative 30; Mismatches 45; Indels 0; Gaps 0;

QY 1 MSLALLPVLASRAVAPAVQALQAGIVGGGEAPRSKMPQVSLRDRYMMHFCG 60
DB 1 MSPPLVLTALALGSLVPSAPQALQAGIVGGGEAPRSKMPQVSLRDRYMMHFCG 60
QY 61 GSIIHPQWVLTAAHCLGPRVQKDLATLRVQLRBNLYYQOQLPVSIIYHPQFYIIQTGTA 120
DB 61 GSIIHPQWVLTAAHCLGPRVQKDLATLRVQLRBNLYYQOQLPVSIIYHPQFYIIQTGTA 120
QY 121 DIALLEBPVNISSRVHTVTLPPASETFPPGMPGCVTWGMDVNDDEPLPPFPPLKQVAV 180
DB 121 DIALLEBPVNISSRVHTVTLPPASETFPPGMPGCVTWGMDVNDDEPLPPFPPLKQVAV 180
QY 181 PIWENHICDAKXHLGAYTGDVRIIRDMLCAGNSQSDSCKDSGGPLVCYKNGTWLQAG 240
DB 181 PIWENHICDAKXHLGAYTGDVRIIRDMLCAGNSQSDSCKDSGGPLVCYKNGTWLQAG 240
QY 241 VVSMDEGCAQPNRPGIYTRVTVYLLDMIHRYVPE 275
DB 241 VVSMDEGCAQPNRPGIYTRVTVYLLDMIHRYVPE 275

RESULT 8

S56160
mast cell tryptase precursor - Mongolian jird
C/Species: Meriones unguiculatus (Mongolian jird)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S56160
R/Murakumo, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.; Ne
Biochem. J. 309, 921-926, 1995
A/Title: Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones ur
A/Reference number: S56160; MUID:95366971; PMID:7639711
A/Accession: S56160
A/Residues: 1-270 <MUR>
A/Molecule type: mRNA
A/Status: preliminary
A/Cross-references: UNIPROT:P50342; EMBL:D31789; NID:g517122; PIND:BA06598.1; PID:g51712;
C/Superfamily: trypsin; trypsin homology
F;26-262/Domain: trypsin homology <TRY>

Query Match 73.4%; Score 1109.5; DB 2; Length 270;
Best Local Similarity 73.3%; Pred. No. 4, 2e-91;
Matches 200; Conservative 22; Mismatches 46; Indels 5; Gaps 2;

QY 1 MSLALLPVLASRAVAPAVQALQAGIVGGGEAPRSKMPQVSLRDRYMMHFCG 60
DB 1 MLKLLALLP--LFSIMHRSPP---LCQEWGIVGGGEAPGNKMPQVSLRANETVRRHFCG 55
QY 61 GSIIHPQWVLTAAHCLGPRVQKDLATLRVQLRBNLYYQOQLPVSIIYHPQFYIIQTGTA 120
DB 56 GSIIHPQWVLTAAHCLGPRVQKDLATLRVQLRBNLYYQOQLPVSIIYHPQFYIIQTGTA 115
QY 121 DIALLEBPVNISSRVHTVTLPPASETFPPGMPGCVTWGMDVNDDEPLPPFPPLKQVAV 180
DB 116 DIALLEBPVNISSRVHTVTLPPASETFPPGMPGCVTWGMDVNDDEPLPPFPPLKQVAV 175
QY 181 PIWENHICDAKXHLGAYTGDVRIIRDMLCAGNSQSDSCKDSGGPLVCYKNGTWLQAG 240
DB 176 PVVENQLCDLTKXHKVYVYGDNIHIVRDMMLCAGNEGSDSCGDSGGPLVCYKNGTWLQAG 235
QY 241 VVSMDEGCAQPNRPGIYTRVTVYLLDMIHRYVPE 273
DB 236 VVSMDEGCAQPNRPGIYTRVTVYLLDMIHRYVPE 268

RESULT 9

JC4171
trypsin (EC 3.4.21.59) precursor - rat
N/Alternate names: mast cell tryptase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C/Accession: JC4171
R/Ide, H.; Itoh, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama, H.; Osada, Y.; Ne
U. Biochem. 118, 210-215, 1995
A/Title: cDNA sequencing and expression of rat mast cell tryptase.
A/Reference number: JC4171; MUID:96015171; PMID:8537314
A/Accession: JC4171
A/Molecule type: mRNA
A/Residues: 1-274 <IDE>
A/Cross-references: UNIPROT:P50343; DDBJ:D38455; NID:g556555; PIND:BA07486.1; PID:g55655;
C/Comment: This enzyme is basically specific for a connective tissue mast cell, it is up-
easing inhibitors.
C/Superfamily: trypsin; trypsin homology
C/Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-29/Domain: activation peptide #status predicted <ACT>
F;30-274/Product: mast cell tryptase #status predicted <MAT>
F;30-266/Domain: trypsin homology <TRY>
F;73,120,223/Active site: His, Asp, Ser #status predicted
F;131/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 73.1%; Score 1105; DB 2; Length 274;
Best Local Similarity 72.0%; Pred. No. 1, 1e-90;

Db 195 DEVIKODMTCAGSEGHDSQMDSGSGLVGRMCKTWIQGVSWGXCQY-NLPGVARYT 253
 QY 262 YYLDWTHVYVKKP 275
 Db 254 SYVSWTHQHPPLSP 267

RESULT 13

prostaasin (EC 3.4.21.-) precursor - human

AS7014

C/Species: Homo sapiens (man)
 C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C/Accession: AS7014; A54866

R/Yu, J.X.; Chao, L.; Chao, J.

J. Biol. Chem. 270, 13483-13489, 1995

A/Title: Molecular cloning, tissue-specific expression, and cellular localization of hum

A/Reference number: AS7014; MUID:95286644; PMID:7768952

A/Accession: AS7014

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-343 <RES>

A/Cross-references: UNIPROT:P016651; GB:L41351; NID:g862304; PIDN:AAQ41759.1; PID:g862305

A/Experimental source: prostate were determined by protein sequencing

A/Note: parts of this sequence were determined by protein sequencing

R/Yu, J.X.; Chao, L.; Chao, J.

J. Biol. Chem. 269, 18843-18848, 1994

A/Title: Prostaasin is a novel human serine proteinase from seminal fluid. Purification,

A/Reference number: A54866; MUID:94308140; PMID:8034638

A/Accession: A54866

A/Molecule type: protein

A/Residues: 45-64 <YUA>

C/Genetics:

A:Gene: GDB:PRSS8

A/Cross-references: GDB:676446; OMIM:600823

A/Map position: 16p11.2-16p11.2

C/Superfamily: trypsin; trypsin homology

C/Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein

F/-32/Domain: signal sequence #status predicted <SIG>

F/33-44,45-343/Product: prostaasin #status predicted <MAT>

F/33-44/Domain: prostaasin heavy chain #status predicted <CH>

F/45-343/Domain: prostaasin heavy chain #status predicted <CH>

F/45-281/Domain: trypsin homology <TRY>

F/323-341/Domain: transmembrane #status predicted <TM>

F/37-154,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted

F/85,134,238/Active site: His, Asp, Ser #status predicted

F/159/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 34.1%; Score 516; DB 1; Length 343;

Best Local Similarity 40.0%; Pred. No. 3,3e-38;

Matches 110; Conservative 42; Mismatches 109; Indels 14; Gaps 8;

4 LLLALLPVLASRAYAARVAPVQLOOGVGGDEAPRSKPMQVSLVRDRYWNHFGSGSL 63

18 LLLVGLLRSTGAEGBARFQVAPQARITGSSAVAVGQFMVQVSTYEG---VHVGSGSL 74

64 IHPQVVLTAACSGRPVQKLATLRVQRLREGHL--YYQD-QLLPVSRRIIVHPQYIIQTGA 120

75 VSWQVWLTAANCF-PEENHKEAVELGAGHQLDYSBDKAVSLTKOIIHPSPV--LQKGS 131

121 --DIALLEFEPNISRVTVMVLPASSETFPPGMCVWTGKDVNDDELPFPFLKQV 178

132 QGGIALLQISRPITFRYTRIPICLPANASFPNGHLCYTGWGHVAPSVSLTPKPLQD 191

179 KVPIMNHICDAKYHIGAYTGDDVRIIRDMLCAG--NSQRDSCKDGSGGLVCKVNGTW 236

192 EVPLISRETNCILYNIDA-KPEEPHFVQEDMVCAIGVGGKDCQGSQSGGLSCVPEGLM 250

237 IQAGVSWDEGCAQPNRPFGITRTVYTYLDMVTHHYV 271

251 YLTGIVSWGDACGARRRPGVYTLASSYASWIOSKV 285

RESULT 14

KHFU1

coagulation factor Xla (EC 3.4.21.27) precursor [validated] - human

N/Alternate names: antihemophilic factor C; plasma thromboplastin antecedent

C/Species: Homo sapiens (man)

C/Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C/Accession: A27431; A00920; A37940

R/Asakai, R.; Davie, E.W.; Chung, D.W.

Biochemistry 26, 7221-7228, 1987

A/Title: Organization of the gene for human factor XI.

A/Reference number: A27431; MUID:88107663; PMID:2827746

A/Accession: A27431

A/Molecule type: DNA

A/Residues: 1-625 <ASA>

A/Cross-references: UNIPROT:P03951; GB:M18295

A/Note: the sequence shown follows the authors' translation

R/Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.

Biochemistry 25, 2417-2424, 1986

A/Title: Amino acid sequence of human factor XI, a blood coagulation factor with four tar

A/Reference number: A00920; MUID:86243360; PMID:3636155

A/Accession: A00920

A/Molecule type: mRNA

A/Residues: 1-625 <FU>

A/Cross-references: GB:M13142; NID:g182832; PIDN:AA52487.1; PID:g182833

R/McMillen, B.A.; Fujikawa, K.; Davie, E.W.

Biochemistry 30, 2056-2060, 1991

A/Title: Location of the disulfide bonds in human coagulation factor XI: the presence of

A/Reference number: A37940; MUID:91152017; PMID:1996667

A/Accession: A37940

A/Molecule type: protein

A/Residues: 28-33,35-49, 'X', 51-55, 'X', 57-63, 70-75, 'X', 77-79, 107-109, 'X', 111-112, 132-139, 'X', 280-282, 'X', 284, 285-297, 313-316, 'X', 318-319, 320-326, 'X', 328-330, 'X', 347-349, 373, 'X', 375;

C/Comment: The proenzyme consists of two identical chains linked by one or more disulfide

he active site, and a heavy chain, which associates with high molecular weight (HMW) kin

C/Genetics:

A:Gene: GDB:F11

A/Cross-references: GDB:119891; OMIM:264900

A/Map position: 4q35-q35

A/Intons: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 526

C/Function:

A/Description: catalyzes the proteolytic activation of coagulation factor IX

C/Superfamily: blood coagulation intrinsic pathway

C/Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydro

F/-18/Domain: signal sequence #status predicted <SIG>

F/19-387/Product: coagulation factor Xla heavy chain #status experimental <HCH>

F/19-108/Domain: apple repeat <AP1>

F/109-198/Domain: apple repeat <AP2>

F/199-288/Domain: apple repeat <AP3>

F/290-379/Domain: apple repeat <AP4>

F/288-625/Product: coagulation factor Xla light chain #status experimental <LCH>

F/388-618/Domain: trypsin homology <TRY>

F/20-103,514-581,571-599/Disulfide bonds: #status predicted

F/46-76,50-56,110-193,136-165,140-146,200-283,226-255,230-236,291-374,317-346,321-327,380

F/90,126,353,450/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/339/Disulfide bonds: interchain #status predicted

F/387-388/Cleavage site: Arg-116 (coagulation factor Xla) #status experimental

F/331,480,575/Active site: His, Asp, Ser #status predicted

F/491/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 31.0%; Score 468; DB 1; Length 625;

Best Local Similarity 39.5%; Pred. No. 1.2e-33;

Matches 98; Conservative 31; Mismatches 91; Indels 28; Gaps 6;

31 IYGGDEAPRSKPMQVSLVRDRYWNHFGSGSLHPQVVLTAACSGRPVQKLATLRVQ- 89

388 IYGTASVRSQEMVQVLTHTTSPTRHLCVGGSIIONQVILTAACF-YGVSPKLRVYS 446

90 --LREQHLYVQQLLPVSRRIIVHPQYIIQTGADIALLEBPVNISSRVHTVMVLPAS 147

447 GILNQSSEIKEDSPFGVQVEIILHDDYKMAESGYDIALKLETTVYVTSQPRICLPKSGD 506

QY 148 TFPFGMPCWVTGMG-----DVDNDELPPPPFLKQVKVIMENHICDAKYLGAAYTD 201
 DB 507 RRVITTDCTWTCMGTRKLRDKIQN-----TLQKAKIPLVTNBEQCKRY----- 550
 QY 202 VRIIRDMLCAGNSQ--RDSCKDGGGGLVCKVNGTWLQAGVVSMBEGCAQPNRPGIYTR 259
 DB 551 GHKITHKMICAGYRGKADCKDGGGLSCGKNEVHMLVGITSMOEGCAQBERGVTYN 610
 QY 260 VTYIYLDWI 267
 DB 611 VVEYVDWI 618

RESULT 15

KOHUP

plasma kallikrein (EC 3.4.21.34) precursor - human
 N:Alternate names: kininogenin; plasma prekallikrein
 C:Species: Homo sapiens (man)
 C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
 C:Accession: A00921; A37939

R:Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
 Biochemistry 25, 2410-2417, 1986

A>Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four
 A:Reference number: A00921; MUID:86243359; PMID:3521732

A:Accession: A00921

A:Molecule type: mRNA

A:Residues: 1-638 <CHU>

A:Cross-References: UNIPROT:P03952; GB:M13143; NID:g190262; PIDN:AA60153.1; PID:g190263
 R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.
 Biochemistry 30, 2050-2056, 1991

A>Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of
 A:Reference number: A37939; MUID:91152016; PMID:1998666

A:Accession: A37939

A:Molecule type: protein

A:Residues: 20-27;40-46,'X',48,'H',50,'X',52-70,'H',75-76,'X',78-80;103-113;131-140;141-
 142;143-144;145-146;147-148;149-150;151-152;153-154;155-156;157-158;159-160;161-162;163-164;165-166;167-168;169-170;171-172;173-174;175-176;177-178;179-180;181-182;183-184;185-186;187-188;189-190;191-192;193-194;195-196;197-198;199-200;201-202;203-204;205-206;207-208;209-210;211-212;213-214;215-216;217-218;219-220;221-222;223-224;225-226;227-228;229-230;231-232;233-234;235-236;237-238;239-240;241-242;243-244;245-246;247-248;249-250;251-252;253-254;255-256;257-258;259-260;261-262;263-264;265-266;267-268;269-270;271-272;273-274;275-276;277-278;279-280;281-282;283-284;285-286;287-288;289-290;291-292;293-294;295-296;297-298;299-300;301-302;303-304;305-306;307-308;309-310;311-312;313-314;315-316;317-318;319-320;321-322;323-324;325-326;327-328;329-330;331-332;333-334;335-336;337-338;339-340;341-342;343-344;345-346;347-348;349-350;351-352;353-354;355-356;357-358;359-360;361-362;363-364;365-366;367-368;369-370;371-372;373-374;375-376;377-378;379-380;381-382;383-384;385-386;387-388;389-390;391-392;393-394;395-396;397-398;399-400;401-402;403-404;405-406;407-408;409-410;411-412;413-414;415-416;417-418;419-420;421-422;423-424;425-426;427-428;429-430;431-432;433-434;435-436;437-438;439-440;441-442;443-444;445-446;447-448;449-450;451-452;453-454;455-456;457-458;459-460;461-462;463-464;465-466;467-468;469-470;471-472;473-474;475-476;477-478;479-480;481-482;483-484;485-486;487-488;489-490;491-492;493-494;495-496;497-498;499-500;501-502;503-504;505-506;507-508;509-510;511-512;513-514;515-516;517-518;519-520;521-522;523-524;525-526;527-528;529-530;531-532;533-534;535-536;537-538;539-540;541-542;543-544;545-546;547-548;549-550;551-552;553-554;555-556;557-558;559-560;561-562;563-564;565-566;567-568;569-570;571-572;573-574;575-576;577-578;579-580;581-582;583-584;585-586;587-588;589-590;591-592;593-594;595-596;597-598;599-600;601-602;603-604;605-606;607-608;609-610;611-612;613-614;615-616;617-618;619-620;621-622;623-624;625-626;627-628;629-630;631-632;633-634;635-636;637-638;639-640;641-642;643-644;645-646;647-648;649-650;651-652;653-654;655-656;657-658;659-660;661-662;663-664;665-666;667-668;669-670;671-672;673-674;675-676;677-678;679-680;681-682;683-684;685-686;687-688;689-690;691-692;693-694;695-696;697-698;699-700;701-702;703-704;705-706;707-708;709-710;711-712;713-714;715-716;717-718;719-720;721-722;723-724;725-726;727-728;729-730;731-732;733-734;735-736;737-738;739-740;741-742;743-744;745-746;747-748;749-750;751-752;753-754;755-756;757-758;759-760;761-762;763-764;765-766;767-768;769-770;771-772;773-774;775-776;777-778;779-780;781-782;783-784;785-786;787-788;789-790;791-792;793-794;795-796;797-798;799-800;801-802;803-804;805-806;807-808;809-810;811-812;813-814;815-816;817-818;819-820;821-822;823-824;825-826;827-828;829-830;831-832;833-834;835-836;837-838;839-840;841-842;843-844;845-846;847-848;849-850;851-852;853-854;855-856;857-858;859-860;861-862;863-864;865-866;867-868;869-870;871-872;873-874;875-876;877-878;879-880;881-882;883-884;885-886;887-888;889-890;891-892;893-894;895-896;897-898;899-900;901-902;903-904;905-906;907-908;909-910;911-912;913-914;915-916;917-918;919-920;921-922;923-924;925-926;927-928;929-930;931-932;933-934;935-936;937-938;939-940;941-942;943-944;945-946;947-948;949-950;951-952;953-954;955-956;957-958;959-960;961-962;963-964;965-966;967-968;969-970;971-972;973-974;975-976;977-978;979-980;981-982;983-984;985-986;987-988;989-990;991-992;993-994;995-996;997-998;999-1000;1001-1002;1003-1004;1005-1006;1007-1008;1009-1010;1011-1012;1013-1014;1015-1016;1017-1018;1019-1020;1021-1022;1023-1024;1025-1026;1027-1028;1029-1030;1031-1032;1033-1034;1035-1036;1037-1038;1039-1040;1041-1042;1043-1044;1045-1046;1047-1048;1049-1050;1051-1052;1053-1054;1055-1056;1057-1058;1059-1060;1061-1062;1063-1064;1065-1066;1067-1068;1069-1070;1071-1072;1073-1074;1075-1076;1077-1078;1079-1080;1081-1082;1083-1084;1085-1086;1087-1088;1089-1090;1091-1092;1093-1094;1095-1096;1097-1098;1099-1100;1101-1102;1103-1104;1105-1106;1107-1108;1109-1110;1111-1112;1113-1114;1115-1116;1117-1118;1119-1120;1121-1122;1123-1124;1125-1126;1127-1128;1129-1130;1131-1132;1133-1134;1135-1136;1137-1138;1139-1140;1141-1142;1143-1144;1145-1146;1147-1148;1149-1150;1151-1152;1153-1154;1155-1156;1157-1158;1159-1160;1161-1162;1163-1164;1165-1166;1167-1168;1169-1170;1171-1172;1173-1174;1175-1176;1177-1178;1179-1180;1181-1182;1183-1184;1185-1186;1187-1188;1189-1190;1191-1192;1193-1194;1195-1196;1197-1198;1199-1200;1201-1202;1203-1204;1205-1206;1207-1208;1209-1210;1211-1212;1213-1214;1215-1216;1217-1218;1219-1220;1221-1222;1223-1224;1225-1226;1227-1228;1229-1230;1231-1232;1233-1234;1235-1236;1237-1238;1239-1240;1241-1242;1243-1244;1245-1246;1247-1248;1249-1250;1251-1252;1253-1254;1255-1256;1257-1258;1259-1260;1261-1262;1263-1264;1265-1266;1267-1268;1269-1270;1271-1272;1273-1274;1275-1276;1277-1278;1279-1280;1281-1282;1283-1284;1285-1286;1287-1288;1289-1290;1291-1292;1293-1294;1295-1296;1297-1298;1299-1300;1301-1302;1303-1304;1305-1306;1307-1308;1309-1310;1311-1312;1313-1314;1315-1316;1317-1318;1319-1320;1321-1322;1323-1324;1325-1326;1327-1328;1329-1330;1331-1332;1333-1334;1335-1336;1337-1338;1339-1340;1341-1342;1343-1344;1345-1346;1347-1348;1349-1350;1351-1352;1353-1354;1355-1356;1357-1358;1359-1360;1361-1362;1363-1364;1365-1366;1367-1368;1369-1370;1371-1372;1373-1374;1375-1376;1377-1378;1379-1380;1381-1382;1383-1384;1385-1386;1387-1388;1389-1390;1391-1392;1393-1394;1395-1396;1397-1398;1399-1400;1401-1402;1403-1404;1405-1406;1407-1408;1409-1410;1411-1412;1413-1414;1415-1416;1417-1418;1419-1420;1421-1422;1423-1424;1425-1426;1427-1428;1429-1430;1431-1432;1433-1434;1435-1436;1437-1438;1439-1440;1441-1442;1443-1444;1445-1446;1447-1448;1449-1450;1451-1452;1453-1454;1455-1456;1457-1458;1459-1460;1461-1462;1463-1464;1465-1466;1467-1468;1469-1470;1471-1472;1473-1474;1475-1476;1477-1478;1479-1480;1481-1482;1483-1484;1485-1486;1487-1488;1489-1490;1491-1492;1493-1494;1495-1496;1497-1498;1499-1500;1501-1502;1503-1504;1505-1506;1507-1508;1509-1510;1511-1512;1513-1514;1515-1516;1517-1518;1519-1520;1521-1522;1523-1524;1525-1526;1527-1528;1529-1530;1531-1532;1533-1534;1535-1536;1537-1538;1539-1540;1541-1542;1543-1544;1545-1546;1547-1548;1549-1550;1551-1552;1553-1554;1555-1556;1557-1558;1559-1560;1561-1562;1563-1564;1565-1566;1567-1568;1569-1570;1571-1572;1573-1574;1575-1576;1577-1578;1579-1580;1581-1582;1583-1584;1585-1586;1587-1588;1589-1590;1591-1592;1593-1594;1595-1596;1597-1598;1599-1600;1601-1602;1603-1604;1605-1606;1607-1608;1609-1610;1611-1612;1613-1614;1615-1616;1617-1618;1619-1620;1621-1622;1623-1624;1625-1626;1627-1628;1629-1630;1631-1632;1633-1634;1635-1636;1637-1638;1639-1640;1641-1642;1643-1644;1645-1646;1647-1648;1649-1650;1651-1652;1653-1654;1655-1656;1657-1658;1659-1660;1661-1662;1663-1664;1665-1666;1667-1668;1669-1670;1671-1672;1673-1674;1675-1676;1677-1678;1679-1680;1681-1682;1683-1684;1685-1686;1687-1688;1689-1690;1691-1692;1693-1694;1695-1696;1697-1698;1699-1700;1701-1702;1703-1704;1705-1706;1707-1708;1709-1710;1711-1712;1713-1714;1715-1716;1717-1718;1719-1720;1721-1722;1723-1724;1725-1726;1727-1728;1729-1730;1731-1732;1733-1734;1735-1736;1737-1738;1739-1740;1741-1742;1743-1744;1745-1746;1747-1748;1749-1750;1751-1752;1753-1754;1755-1756;1757-1758;1759-1760;1761-1762;1763-1764;1765-1766;1767-1768;1769-1770;1771-1772;1773-1774;1775-1776;1777-1778;1779-1780;1781-1782;1783-1784;1785-1786;1787-1788;1789-1790;1791-1792;1793-1794;1795-1796;1797-1798;1799-1800;1801-1802;1803-1804;1805-1806;1807-1808;1809-1810;1811-1812;1813-1814;1815-1816;1817-1818;1819-1820;1821-1822;1823-1824;1825-1826;1827-1828;1829-1830;1831-1832;1833-1834;1835-1836;1837-1838;1839-1840;1841-1842;1843-1844;1845-1846;1847-1848;1849-1850;1851-1852;1853-1854;1855-1856;1857-1858;1859-1860;1861-1862;1863-1864;1865-1866;1867-1868;1869-1870;1871-1872;1873-1874;1875-1876;1877-1878;1879-1880;1881-1882;1883-1884;1885-1886;1887-1888;1889-1890;1891-1892;1893-1894;1895-1896;1897-1898;1899-1900;1901-1902;1903-1904;1905-1906;1907-1908;1909-1910;1911-1912;1913-1914;1915-1916;1917-1918;1919-1920;1921-1922;1923-1924;1925-1926;1927-1928;1929-1930;1931-1932;1933-1934;1935-1936;1937-1938;1939-1940;1941-1942;1943-1944;1945-1946;1947-1948;1949-1950;1951-1952;1953-1954;1955-1956;1957-1958;1959-1960;1961-1962;1963-1964;1965-1966;1967-1968;1969-1970;1971-1972;1973-1974;1975-1976;1977-1978;1979-1980;1981-1982;1983-1984;1985-1986;1987-1988;1989-1990;1991-1992;1993-1994;1995-1996;1997-1998;1999-2000;2001-2002;2003-2004;2005-2006;2007-2008;2009-2010;2011-2012;2013-2014;2015-2016;2017-2018;2019-2020;2021-2022;2023-2024;2025-2026;2027-2028;2029-2030;2031-2032;2033-2034;2035-2036;2037-2038;2039-2040;2041-2042;2043-2044;2045-2046;2047-2048;2049-2050;2051-2052;2053-2054;2055-2056;2057-2058;2059-2060;2061-2062;2063-2064;2065-2066;2067-2068;2069-2070;2071-2072;2073-2074;2075-2076;2077-2078;2079-2080;2081-2082;2083-2084;2085-2086;2087-2088;2089-2090;2091-2092;2093-2094;2095-2096;2097-2098;2099-2100;2101-2102;2103-2104;2105-2106;2107-2108;2109-2110;2111-2112;2113-2114;2115-2116;2117-2118;2119-2120;2121-2122;2123-2124;2125-2126;2127-2128;2129-2130;2131-2132;2133-2134;2135-2136;2137-2138;2139-2140;2141-2142;2143-2144;2145-2146;2147-2148;2149-2150;2151-2152;2153-2154;2155-2156;2157-2158;2159-2160;2161-2162;2163-2164;2165-2166;2167-2168;2169-2170;2171-2172;2173-2174;2175-2176;2177-2178;2179-2180;2181-2182;2183-2184;2185-2186;2187-2188;2189-2190;2191-2192;2193-2194;2195-2196;2197-2198;2199-2200;2201-2202;2203-2204;2205-2206;2207-2208;2209-2210;2211-2212;2213-2214;2215-2216;2217-2218;2219-2220;2221-2222;2223-2224;2225-2226;2227-2228;2229-2230;2231-2232;2233-2234;2235-2236;2237-2238;2239-2240;2241-2242;2243-2244;2245-2246;2247-2248;2249-2250;2251-2252;2253-2254;2255-2256;2257-2258;2259-2260;2261-2262;2263-2264;2265-2266;2267-2268;2269-2270;2271-2272;2273-2274;2275-2276;2277-2278;2279-2280;2281-2282;2283-2284;2285-2286;2287-2288;2289-2290;2291-2292;2293-2294;2295-2296;2297-2298;2299-2300;2301-2302;2303-2304;2305-2306;2307-2308;2309-2310;2311-2312;2313-2314;2315-2316;2317-2318;2319-2320;2321-2322;2323-2324;2325-2326;2327-2328;2329-2330;2331-2332;2333-2334;2335-2336;2337-2338;2339-2340;2341-2342;2343-2344;2345-2346;2347-2348;2349-2350;2351-2352;2353-2354;2355-2356;2357-2358;2359-2360;2361-2362;2363-2364;2365-2366;2367-2368;2369-2370;2371-2372;2373-2374;2375-2376;2377-2378;2379-2380;2381-2382;2383-2384;2385-2386;2387-2388;2389-2390;2391-2392;2393-2394;2395-2396;2397-2398;2399-2400;2401-2402;2403-2404;2405-2406;2407-2408;2409-2410;2411-2412;2413-2414;2415-2416;2417-2418;2419-2420;2421-2422;2423-2424;2425-2426;2427-2428;2429-2430;2431-2432;2433-2434;2435-2436;2437-2438;2439-2440;2441-2442;2443-2444;2445-2446;2447-2448;2449-2450;2451-2452;2453-2454;2455-2456;2457-2458;2459-2460;2461-2462;2463-2464;2465-2466;2467-2468;2469-2470;2471-2472;2473-2474;2475-2476;2477-2478;2479-2480;2481-2482;2483-2484;2485-2486;2487-2488;2489-2490;2491-2492;2493-2494;2495-2496;2497-2498;2499-2500;2501-2502;2503-2504;2505-2506;2507-2508;2509-2510;2511-2512;2513-2514;2515-2516;2517-2518;2519-

This page blank (optional)

	-1-	CATALYTIC ACTIVITY:	Preferential cleavage: Arg- --, Lys- -, but
CC	-1-	with more restricted specificity than trypsin.	
CC	-1-	SUBUNIT:	Homotrimer.
CC	-1-	SUBCELLULAR LOCATION:	Released from the secretory granules upon
CC	-1-	mast cell activation.	
CC	-1-	ALTERNATIVE PRODUCTS:	
CC	-1-	Event=Alternative splicing; Named isoforms=2;	
CC	Name=1;		
CC	IsoId=P15157-1;	Sequence=Displayed;	
CC	Name=2;		
CC	IsoId=P15157-2;	Sequence=VSP_005374;	
CC	-1-	SIMILARITY:	Belongs to the peptidase S1 family. Trypsase
CC	subfamily.		
CC	-		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration -		
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-		
DR	EMBL;	M30038;	AA06934.1; -
DR	EMBL;	AF098328;	AAD17846.1; -
DR	EMBL;	AF206665;	AAG35695.1; -
DR	EMBL;	AF206666;	AAG35696.1; -
DR	PDB;	1LTO;	X-ray; A/B/C/D=31-275.
DR	MEROPS;	S01.143;	-
DR	GeneW;	HGNC:12018;	TPS1.
DR	MIM;	191080;	-
DR	GO;	GO:0008236;	F:serine-type peptidase activity; TAS.
DR	GO;	GO:0006952;	P:defense response; TAS.
DR	InterPro;	IPR009003;	Pept_Ser_Cys.
DR	InterPro;	IPR001254;	Peptidase_S1.
DR	InterPro;	IPR001314;	Peptidase_S1A.
DR	Pfam;	PF00089;	Tyrsin_1.
DR	PRINTS;	PR00722;	CHYMOTRYPSIN.
DR	SMART;	SMO02020;	Tryp_Spec_1.
DR	PROSITE;	PS50240;	TRYPSIN_DOM; 1.
DR	PROSITE;	PS00134;	TRYPSIN_HIS; 1.
KM	PROSITE;	PS00135;	TRYPSIN_SER; 1.
KM	3D-structure;	Alternative splicing; Direct protein sequencing;	
KM	Glycoprotein;	Hydrolase; Polymorphism; Serine protease; Signal;	
KM	Zymoetial.		
FT	SIGNAL	1	18 Potential.
FT	PROPEP	19	30 Activation peptide.
FT	CHAIN	31	275 Alpha-trypase.
FT	ACT_SITE	74	74 Charge relay system.
FT	ACT_SITE	121	121 Charge relay system.
FT	ACT_SITE	224	224 Charge relay system.
FT	DISULFID	59	75
FT	DISULFID	155	230
FT	DISULFID	188	211
FT	DISULFID	220	248
FT	CARBOHYD	132	132
FT	CARBOHYD	233	233
FT	VASPLIC	79	87
FT			N-linked (GLCNAC . .) (Potential)
FT			N-linked (GLCNAC . .) (Potential)
FT			Misling (in Isoform 2).
FT			/FTId=VSP_005374.
FT	VARIANT	15	15 R -> P (in alpha-II)
FT			/FTId=VAR_012102.
FT	VARIANT	221	221 K -> Q (in alpha-II; dbSNP:1137382).
FT			/FTId=VAR_012103.
FT	SEQUENCE	275 AA;	30772 MW; B9BAC4BBBCB9ICE75 CRC64;
FT	CONFLICT	215	216
FT	BEET LOCAL SIMILARITY	99.5%;	Score 1505; DB 1; Length 275;
FT	Matches	273;	Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY	1	MLSLILLALPYLASRAIYAAPAVQALQAGIVGGGEAEFRSKWPQOVSLRVDRIRYMAFCG	60
OY	1	MLSLILLALPYLASRAIYAAPAVQALQAGIVGGGEAEFRSKWPQOVSLRVDRIRYMAFCG	60

QY	6	GSIIHQWLTAAHCGPVPKDLATFLQLEHQLYYODOLPFSRIIYHPQFIYIQTGA	120
Db	61	GSIIHQWLTAAHCGPVPKDLATFLQLEHQLYYODOLPFSRIIYHPQFIYIQTGA	120
QY	121	DIALLEBPVNISSRVHTVMLPPASETFPPGMCWYTGWDVNDDEPLPPPPPKOVKV	180
Db	121	DIALLEBPVNISSRVHTVMLPPASETFPPGMCWYTGWDVNDDEPLPPPPPKOVKV	180
QY	181	PIEMENNICAKYHGLGATYGDVRIIRDMLCAGNSORDSCKGSGGFLYCKNAGTWLOAG	240
Db	181	PIEMENNICAKYHGLGATYGDVRIIRDMLCAGNIRSDCKGSGGFLYCKNAGTWLOAG	240
QY	241	VWSWDEGCAQPNRPGLYTRVITYYLDWIIHHVYPKKP	275
Db	241	VWSWDEGCAQPNRPGLYTRVITYYLDWIIHHVYPKKP	275
RESULT 2			
Q86TM8	086TM8	PRELIMINARY;	PRT; 275 AA.
AC	086TM8;		
ID	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	TSPI protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Bueckow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatcenco U., Marusina K., Farmer A.A., Riddin G.M., Hong L.,		
RA	Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaefer T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshlyuk S., Carantini P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., Mcowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,		
RA	Krzywniaki M.I., Skalska U., Smailus D.E., Schermer A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Brain;		
RC	Strausberg R.;		
CC	Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: Belongs to peptidase family SL.		
DR	EMBL; BC028059; AAH28059.1; -		
DR	HSSP; P15157; ILTO.		
DR	GO; GO:0004263; F:phosphatase activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004295; F:trypsin activity; IEA.		
DR	GO; GO:0006508; F:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001342; Peptidase SL.		
DR	InterPro; IPR001314; Peptidase SL.		
DR	InterPro; IPR009003; Pept_Ser_Cys.		
DR	Pfam; PF00089; Trypsin; 1		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	SMART; SM00020; TRY_P_Spec. 1.		
DR	PROSITE; PS50240; TRYPSIN_DOM. 1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.		

DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 275 AA; 30713 MW; 189C3BBCB473FA3 CRC64;
 Query Match 98.8%; Score 1494; DB 2; Length 275;
 Best Local Similarity 98.5%; Pred. No. 1,4e-12;
 Matches 271; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTLLALPYLASRAYAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMHFCG 60
 |||||
 DB 1 MLSTLLALPYLASRAYAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMHFCG 60
 |||||
 QY 61 GSLIHPQWVLTAAHCLGPVDVLTALRVQLREQHLYYQDQLLPVSRILVHPQFYIIQTGA 120
 |||||
 DB 61 GSLIHPQWVLTAAHCLGPVDVLTALRVQLREQHLYYQDQLLPVSRILVHPQFYIIQTGA 120
 |||||
 QY 121 DIALLEPEPNISSRVHTVWLPPASETFPPGMPGCMVTGMDGVNDDEPLPPFPKQYKV 180
 |||||
 DB 121 DIALLEPEPNISSRVHTVWLPPASETFPPGMPGCMVTGMDGVNDDEPLPPFPKQYKV 180
 |||||
 QY 181 PIMENHICDAKYHLAGYTGDDVRIIRDMLCAGNSQSDSCGDSGGPLVCVNGTWLQAG 240
 |||||
 DB 181 PIMENHICDAKYHLAGYTGDDVRIIRDMLCAGNTRRDSQCGDSGGPLVCVNGTWLQAG 240
 |||||
 QY 241 VVSWDEGCAQPNRPQIYTRVITYYLDWIHHYVPKRP 275
 |||||
 DB 241 VVSWDEGCAQPNRPQIYTRVITYYLDWIHHYVPKRP 275
 |||||

RESULT 3
 Q86U5 PRELIMINARY; PRT; 276 AA.
 ID Q86U5;
 AC Q86U5;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE TP51 protein (Fragment).
 GN Name=TP51;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci R.D., Mullahy S.J.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Gumaratne P.H.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 Villalón D.K., Muzny D.M., Sodergren E., Madan A., Rodriguez S., Sanchez A.,
 Fahy J., Helton E., Ketterman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz D.E., Myers R.M., Buterfield Y.S.,
 Krzywinski M.I., Skalek J., Smailus D.E., Scherch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX Strausberg R.;
 Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family 11.
 EMBL; BC051852; AAH51852.1; -.

DR HSP; P15157; ILTO.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004293; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 FT NON TER
 SQ SEQUENCE 276 AA; 30869 MW; 8CDC5EA037955F9C CRC64;
 Query Match 98.8%; Score 1494; DB 2; Length 276;
 Best Local Similarity 98.5%; Pred. No. 1,4e-12;
 Matches 271; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTLLALPYLASRAYAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMHFCG 60
 |||||
 DB 2 MLSTLLALPYLASRAYAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMHFCG 61
 |||||
 QY 61 GSLIHPQWVLTAAHCLGPVDVLTALRVQLREQHLYYQDQLLPVSRILVHPQFYIIQTGA 120
 |||||
 DB 62 GSLIHPQWVLTAAHCLGPVDVLTALRVQLREQHLYYQDQLLPVSRILVHPQFYIIQTGA 121
 |||||
 QY 121 DIALLEPEPNISSRVHTVWLPPASETFPPGMPGCMVTGMDGVNDDEPLPPFPKQYKV 180
 |||||
 DB 122 DIALLEPEPNISSRVHTVWLPPASETFPPGMPGCMVTGMDGVNDDEPLPPFPKQYKV 181
 |||||
 QY 181 PIMENHICDAKYHLAGYTGDDVRIIRDMLCAGNSQSDSCGDSGGPLVCVNGTWLQAG 240
 |||||
 DB 182 PIMENHICDAKYHLAGYTGDDVRIIRDMLCAGNTRRDSQCGDSGGPLVCVNGTWLQAG 241
 |||||
 QY 241 VVSWDEGCAQPNRPQIYTRVITYYLDWIHHYVPKRP 275
 |||||
 DB 242 VVSWDEGCAQPNRPQIYTRVITYYLDWIHHYVPKRP 276
 |||||

RESULT 4
 Q8B051 PRELIMINARY; PRT; 275 AA.
 ID Q8B051;
 AC Q8B051;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Beta tryptase 1.
 GN Name=TP5B1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled tissue;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci R.D., Mullahy S.J.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Gumaratne P.H.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 Villalón D.K., Muzny D.M., Sodergren E., Madan A., Rodriguez S., Sanchez A.,
 Fahy J., Helton E., Ketterman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Poled tissue;
 RA Director MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL: BC074975; AAF74975.1; -;
 DR GO: GO:0004263; F:chymotrypsin activity; IEA.
 DR GO: GO:0004295; F:trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR009003; Pept_Ser_Cys.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP SPc; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR HydroLase; Protease; Serine protease.
 KW SEQUENCE 275 AA; 30488 MW; A8F0B12C58F86C12 CRC64;

Query Match 93.5%; Score 1414; DB 2; Length 275;

Best Local Similarity 92.7%; Pred. No. 1,3e-114;
 Matches 255; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSLILLALPVLASRAVAPVQALQAGIVGGGEAPRSKMPQVSLVRDRYMMHFCG 60
 DB 1 MSLILLALPVLASRAVAPVQALQAGIVGGGEAPRSKMPQVSLVRDRYMMHFCG 60
 QY 61 GSLIHPQWLTAAHCGIPVYKDIATLRVLRQHLTYQDQLIPVSRIVHPQFYIIQTGA 120
 DB 61 GSLIHPQWLTAAHCGIPVYKDIATLRVLRQHLTYQDQLIPVSRIVHPQFYIIQTGA 120
 QY 121 DIALLELEPPVNISSVHTVTLPPASERPPGMPGVTGMDVNDERLPPRPPLKQKV 180
 DB 121 DIALLELEPPVNISSVHTVTLPPASERPPGMPGVTGMDVNDERLPPRPPLKQKV 180
 QY 181 PTMENHICDAKATLGAYTGDVRIIRDDMLCAGNSQSDSCKDSGGPLVCKVNGTWLQAG 240
 DB 181 PTMENHICDAKATLGAYTGDVRIIRDDMLCAGNSQSDSCKDSGGPLVCKVNGTWLQAG 240
 QY 241 VVSWDEGCAQPNRPGIYTRVTTYLLDMIHVYPKKP 275
 DB 241 VVSWDEGCAQPNRPGIYTRVTTYLLDMIHVYPKKP 275
 QY 241 VVSWDEGCAQPNRPGIYTRVTTYLLDMIHVYPKKP 275
 DB 241 VVSWDEGCAQPNRPGIYTRVTTYLLDMIHVYPKKP 275

RESULT 5

TRBI_HUMAN STANDARD; PRT; 275 AA.
 ID TRBI_HUMAN Q15661; Q9H2Y4;
 AC Q15661; Q9H2Y4; Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Trypsin beta-1 precursor (EC 3.4.21.59) (Trypsin 1) (Trypsin I).
 GN Name=TPSBI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=90251647; PubMed=2187193;
 RA Vanderlisse P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
 RA Caughey G.H.;
 RT "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene

RT serine protease family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99121069; PubMed=9920877; DOI=10.1074/jbc.274.6.3355;
 RA Pallaro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
 RT "Characterization of genes encoding known and novel human mast cell
 RT tryptases on chromosome 16p13.3.";
 RL J. Biol. Chem. 274:3355-3362(1999).
 RN [3]
 RP SEQUENCE OF 54-275 FROM N.A. (ISOFORM 2).
 RA Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J.,
 RA Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
 RA Hunt J.E.;
 RT "Molecular cloning and characterization of novel human tryptase cDNAs
 RT and splicing variants.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Trypsin is the major neutral protease present in mast
 CC cells and is secreted upon the coupled activation-degranulation
 CC response of this cell type.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Released from the secretory granules upon
 CC mast cell activation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q15661-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q15661-2; Sequence=VSP_005375;
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Trypsin
 CC subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M33494; AAC83172.1; -;
 DR EMBL: M33491; AAA36778.1; -;
 DR EMBL: AF099144; AAD17860.1; -;
 DR EMBL: AF206667; AAC35697.1; -;
 DR PIR: A35863; A35863.
 DR HSSP: P20231; 1A0L.
 DR MEROPS: S01.015; -;
 DR MEROPS: S01.242; -;
 DR Genew; HGNC:12019; TPSBI.
 DR MIM: 191081; -;
 DR InterPro: IPR009003; Pept_Ser_Cys.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP SPc; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Alternative splicing; Glycoprotein; Hydrolase; Polymorphism;
 KW Serine protease; Signal; Zymogen.
 FT SIGNAL 1 18
 FT PROPEP 19 30 Potential.
 FT CHAIN 31 275 Activation peptide (By similarity).
 FT ACT_SITE 74 74 Trypsin beta-1.
 FT ACT_SITE 121 121 Charge relay system.
 FT ACT_SITE 224 224 Charge relay system.
 FT DISULFID 59 75 Charge relay system.
 FT DISULFID 155 230 By similarity.
 FT DISULFID 188 211 By similarity.
 FT DISULFID 220 248 By similarity.
 FT By similarity.

FT	CARBOHYD	132	132	N-linked (GlcNAc. . .) (Potential).
FT <td>CARBOHYD</td> <td>233</td> <td>233</td> <td>N-linked (GlcNAc. . .) (Potential).</td>	CARBOHYD	233	233	N-linked (GlcNAc. . .) (Potential).
FT <td>VARSPLIC</td> <td>79</td> <td>87</td> <td>Missing (in isoform 2).</td>	VARSPLIC	79	87	Missing (in isoform 2).
FT <td>VARIANT</td> <td>18</td> <td>18</td> <td>A->V (1in dbSNP:005375).</td>	VARIANT	18	18	A->V (1in dbSNP:005375).
FT <td>VARIANT</td> <td>18</td> <td>18</td> <td>A->V (1in dbSNP:1800984).</td>	VARIANT	18	18	A->V (1in dbSNP:1800984).
FT <td>VARIANT</td> <td>23</td> <td>23</td> <td>/FTID=VAR 014557.</td>	VARIANT	23	23	/FTID=VAR 014557.
FT <td>VARIANT</td> <td>85</td> <td>85</td> <td>G->V (1in dbSNP:1800986).</td>	VARIANT	85	85	G->V (1in dbSNP:1800986).
FT <td>VARIANT</td> <td>132</td> <td>132</td> <td>/FTID=VAR 014558.</td>	VARIANT	132	132	/FTID=VAR 014558.
FT <td>VARIANT</td> <td>132</td> <td>132</td> <td>A->T (1in dbSNP:2234902).</td>	VARIANT	132	132	A->T (1in dbSNP:2234902).
FT <td>VARIANT</td> <td>141</td> <td>141</td> <td>/FTID=VAR 014559.</td>	VARIANT	141	141	/FTID=VAR 014559.
FT <td>VARIANT</td> <td>162</td> <td>162</td> <td>N->K (1in dbSNP:1800991).</td>	VARIANT	162	162	N->K (1in dbSNP:1800991).
FT <td>VARIANT</td> <td>170</td> <td>170</td> <td>/FTID=VAR 016102.</td>	VARIANT	170	170	/FTID=VAR 016102.
FT <td>VARIANT</td> <td>215</td> <td>215</td> <td>T->A (1in dbSNP:1800992).</td>	VARIANT	215	215	T->A (1in dbSNP:1800992).
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014560.</td>	VARIANT	216	216	/FTID=VAR 014560.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>D->N (1in dbSNP:2234641).</td>	VARIANT	216	216	D->N (1in dbSNP:2234641).
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014561.</td>	VARIANT	216	216	/FTID=VAR 014561.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>P->S (1in dbSNP:2234904).</td>	VARIANT	216	216	P->S (1in dbSNP:2234904).
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014562.</td>	VARIANT	216	216	/FTID=VAR 014562.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>T->S (1in dbSNP:2234905).</td>	VARIANT	216	216	T->S (1in dbSNP:2234905).
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014563.</td>	VARIANT	216	216	/FTID=VAR 014563.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>R->Q (1in dbSNP:2234906).</td>	VARIANT	216	216	R->Q (1in dbSNP:2234906).
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014564.</td>	VARIANT	216	216	/FTID=VAR 014564.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014565.</td>	VARIANT	216	216	/FTID=VAR 014565.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014566.</td>	VARIANT	216	216	/FTID=VAR 014566.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014567.</td>	VARIANT	216	216	/FTID=VAR 014567.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014568.</td>	VARIANT	216	216	/FTID=VAR 014568.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014569.</td>	VARIANT	216	216	/FTID=VAR 014569.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014570.</td>	VARIANT	216	216	/FTID=VAR 014570.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014571.</td>	VARIANT	216	216	/FTID=VAR 014571.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014572.</td>	VARIANT	216	216	/FTID=VAR 014572.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014573.</td>	VARIANT	216	216	/FTID=VAR 014573.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014574.</td>	VARIANT	216	216	/FTID=VAR 014574.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014575.</td>	VARIANT	216	216	/FTID=VAR 014575.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014576.</td>	VARIANT	216	216	/FTID=VAR 014576.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014577.</td>	VARIANT	216	216	/FTID=VAR 014577.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014578.</td>	VARIANT	216	216	/FTID=VAR 014578.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014579.</td>	VARIANT	216	216	/FTID=VAR 014579.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014580.</td>	VARIANT	216	216	/FTID=VAR 014580.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014581.</td>	VARIANT	216	216	/FTID=VAR 014581.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014582.</td>	VARIANT	216	216	/FTID=VAR 014582.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014583.</td>	VARIANT	216	216	/FTID=VAR 014583.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014584.</td>	VARIANT	216	216	/FTID=VAR 014584.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014585.</td>	VARIANT	216	216	/FTID=VAR 014585.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014586.</td>	VARIANT	216	216	/FTID=VAR 014586.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014587.</td>	VARIANT	216	216	/FTID=VAR 014587.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014588.</td>	VARIANT	216	216	/FTID=VAR 014588.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014589.</td>	VARIANT	216	216	/FTID=VAR 014589.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014590.</td>	VARIANT	216	216	/FTID=VAR 014590.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014591.</td>	VARIANT	216	216	/FTID=VAR 014591.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014592.</td>	VARIANT	216	216	/FTID=VAR 014592.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014593.</td>	VARIANT	216	216	/FTID=VAR 014593.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014594.</td>	VARIANT	216	216	/FTID=VAR 014594.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014595.</td>	VARIANT	216	216	/FTID=VAR 014595.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014596.</td>	VARIANT	216	216	/FTID=VAR 014596.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014597.</td>	VARIANT	216	216	/FTID=VAR 014597.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014598.</td>	VARIANT	216	216	/FTID=VAR 014598.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014599.</td>	VARIANT	216	216	/FTID=VAR 014599.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014600.</td>	VARIANT	216	216	/FTID=VAR 014600.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014601.</td>	VARIANT	216	216	/FTID=VAR 014601.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014602.</td>	VARIANT	216	216	/FTID=VAR 014602.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014603.</td>	VARIANT	216	216	/FTID=VAR 014603.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014604.</td>	VARIANT	216	216	/FTID=VAR 014604.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014605.</td>	VARIANT	216	216	/FTID=VAR 014605.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014606.</td>	VARIANT	216	216	/FTID=VAR 014606.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014607.</td>	VARIANT	216	216	/FTID=VAR 014607.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014608.</td>	VARIANT	216	216	/FTID=VAR 014608.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014609.</td>	VARIANT	216	216	/FTID=VAR 014609.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014610.</td>	VARIANT	216	216	/FTID=VAR 014610.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014611.</td>	VARIANT	216	216	/FTID=VAR 014611.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014612.</td>	VARIANT	216	216	/FTID=VAR 014612.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014613.</td>	VARIANT	216	216	/FTID=VAR 014613.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014614.</td>	VARIANT	216	216	/FTID=VAR 014614.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014615.</td>	VARIANT	216	216	/FTID=VAR 014615.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014616.</td>	VARIANT	216	216	/FTID=VAR 014616.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014617.</td>	VARIANT	216	216	/FTID=VAR 014617.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014618.</td>	VARIANT	216	216	/FTID=VAR 014618.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014619.</td>	VARIANT	216	216	/FTID=VAR 014619.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014620.</td>	VARIANT	216	216	/FTID=VAR 014620.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014621.</td>	VARIANT	216	216	/FTID=VAR 014621.
FT <td>VARIANT</td> <td>216</td> <td>216</td> <td>/FTID=VAR 014622.</td>	VARIANT	216	216	/FTID=VAR 014622.
FT <td>VARIANT</td>	VARIANT			

RA Blom T., Hellman L.;
RT "Characterization of a tryptase mRNA expressed in the human basophil
RL cell line K0812.";
RN Scand. J. Immunol. 37:203-208(1993).
RP [3]
RX SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3).
RA MEDLINE=90251647; PubMed=2187193;
RX Vanderheide P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
RA Caughey G.H.;
RT "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene
RL RT serine protease family.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
RP [4]
RX SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3).
RA MEDLINE=99121069; PubMed=9920877; DOI=10.1074/jbc.274.6.3355;
RX Pallaoero M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RT "Characterization of genes encoding known and novel human mast cell
RL tryptases on chromosome 16p13.3.";
RN J. Biol. Chem. 274:3355-3362(1999).
RP [5]
RX REVISIONS.
RA Pallaoero M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RL Submitted (OCT-2001) to the EMBL/genbank/DBJ databases.
RN [6]
RX SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Mang J., Hatien F.,
RA DiChienko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uden T.B., Toshiyuki S., Carinini P., Prange C.,
RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Scherf A.C., Schein J.E., Jones S.J.M., Skalski A., Smalios D.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16939-16903(2002).
RP [7]
RX X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RN MEDLINE=98180625; PubMed=9521139; DOI=10.1038/32703;
RX Pereira P.J.B., Bergner A., Macedo-Ribeiro S., Huber R.,
RA Matschinger G., Fritz H., Sommerhoff C.P., Bode W.;
RT "Human beta-tryptase is a ring-like tetramer with active sites facing
RL a central pore.";
RN Nature 392:306-311(1998).
RP [8]
RX X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
RN MEDLINE=99432166; PubMed=10500112; DOI=10.1073/pnas.96.20.10984;
RX Sommerhoff C.P., Bode W., Pereira P.J.B., Stubbs M.T.,
RA Stuerzbecher U., Plehoczka G.P., Matschinger G., Bergner A.;
RT "The structure of the human beta-1-tryptase tetramer: fo(u)r better or
RL worse.";
RN Proc. Natl. Acad. Sci. U.S.A. 96:10984-10991(1999).
RP [9]
RX FUNCTION: Tryptase is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -1 CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|- , but
CC with more restricted specificity than trypsin.
CC -1 SUBUNIT: Homotetramer.
CC -1 SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -1 POLYMORPHISM: There are two alleles, beta-II and beta-III which
CC differ by 3 residues.

CC -! SIMILARITY: Belongs to the peptidase S1 family. Trypsase
 CC subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M37486; AAA51843.1; -;
 DR EMBL: M37492; AAA56779.1; -;
 DR EMBL: M37493; AAA36780.1; -;
 DR EMBL: S55551; AAD13876.1; -;
 DR EMBL: AF099143; AAD17859.2; -;
 DR EMBL: AF099145; AAD17857.1; -;
 DR EMBL: AF099146; AAD17858.1; -;
 DR EMBL: BC029356; AAH29356.1; -;
 DR PIR: B35863; B35863.
 DR PDB: 1AOL; X-ray; A/B/C/D=31-274.
 DR PDB: 1AAO; Model; @=31-275.
 DR MEROPS: S01.242; -;
 DR Genew; HGNC:14120; TP5B2.
 DR H-InvDB; HIX0012676; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR 3D-structure; Glycoprotein; Hydrolase; Polymorphism; Serine protease;
 KW Signal; Zymogen.
 FT SIGNAL 1 18
 FT PROPEP 19 30
 FT CHAIN 31 275
 FT ACT_SITE 74 74
 FT ACT_SITE 121 121
 FT ACT_SITE 224 224
 FT DISULFID 59 75
 FT DISULFID 155 230
 FT DISULFID 188 211
 FT DISULFID 220 248
 FT CARBOHYD 233 233
 FT VARIANT 51 53
 FT CONFLICT 132 132
 FT STRAND 32 32
 FT STRAND 35 36
 FT TURN 39 40
 FT TURN 43 44
 FT STRAND 45 51
 FT STRAND 55 65
 FT TURN 66 67
 FT STRAND 68 71
 FT HELIX 73 75
 FT TURN 76 76
 FT STRAND 79 79
 FT HELIX 83 85
 FT STRAND 86 90
 FT STRAND 94 94
 FT TURN 95 98
 FT STRAND 102 102
 FT STRAND 104 109
 FT TURN 111 112
 FT HELIX 116 118
 FT STRAND 123 127

N-linked (GlcNAc..) (Potential).
 HGP -> RDR (in beta-III).
 /Frid=VAR 012104.
 K -> N (in Ref. 3).

FT STRAND 141 141
 FT TURN 145 146
 FT TURN 151 152
 FT STRAND 155 159
 FT STRAND 164 164
 FT TURN 165 166
 FT STRAND 167 167
 FT TURN 171 172
 FT STRAND 174 174
 FT STRAND 176 180
 FT STRAND 182 183
 FT HELIX 185 191
 FT TURN 192 195
 FT STRAND 196 196
 FT TURN 200 201
 FT TURN 207 208
 FT STRAND 209 212
 FT STRAND 214 214
 FT TURN 215 216
 FT STRAND 217 218
 FT TURN 221 222
 FT TURN 224 225
 FT STRAND 227 232
 FT TURN 233 234
 FT STRAND 235 244
 FT STRAND 250 250
 FT TURN 251 252
 FT STRAND 253 253
 FT STRAND 255 259
 FT HELIX 260 263
 FT HELIX 264 270
 SQ SEQUENCE 275 AA; 30529 MW; 2B27396C51F5C7A0 CRC64;

Query Match 92.9%; Score 1405; DB 1; Length 275;
 Best Local Similarity 92.0%; Pred. No. 7.7e-114;
 Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MISLILLALPVLSAAYAPAPVQALQAGIVGQGEAPRSKPMQVSLRVDRIYMAHFCG 60
 1 MNLILLALLPVLSAAYAPAPVQALQAGIVGQGEAPRSKPMQVSLRVDRIYMAHFCG 60
 DB 61 GSLIHPOVNLTAHAGLGPVDVLAATRLVQLREOHLYYQDOLLPVSRILVHPOFYILQGA 120
 61 GSLIHPOVNLTAHAGLGPVDVLAATRLVQLREOHLYYQDOLLPVSRILVHPOFYILQGA 120
 DB 121 DIALLELEBPVNISSRVHTVMLPPASETFPPGMPQVWGMDVDNDEPLPPFPPLKQYKV 180
 121 DIALLELEBPVNISSRVHTVMLPPASETFPPGMPQVWGMDVDNDEPLPPFPPLKQYKV 180
 QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNSQORDSCKDSGGPLVCVNGTWLQAG 240
 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNTRBDSCKDSGGPLVCVNGTWLQAG 240
 DB 241 VVSWDEGCAQPRRPGITRYRTVITYLDIMHHVYPKKP 275
 241 VVSWDEGCAQPRRPGITRYRTVITYLDIMHHVYPKKP 275
 QY 241 VVSWDEGCAQPRRPGITRYRTVITYLDIMHHVYPKKP 275
 241 VVSWDEGCAQPRRPGITRYRTVITYLDIMHHVYPKKP 275
 DB 241 VVSWDEGCAQPRRPGITRYRTVITYLDIMHHVYPKKP 275
 241 VVSWDEGCAQPRRPGITRYRTVITYLDIMHHVYPKKP 275

RESULT 7
 Q6NZY1 PRELIMINARY; PRT; 282 AA.
 AC Q6NZY1; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE TP5B2 protein.
 GN Name=TP5B2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX MEDLINE=2238857; Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strassberg R.L., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Klausner R.D., Zeeberg B., Buecaw K.H., Scheffer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buecaw K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villard S., Morley K.C., Hale A.M., Gay L.J., Huijck S.W.,
 RA Richardson D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green S.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska J., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP TISSUE=Brain;
 RC SEQUENCE FROM N.A.
 RA Director MGC Project;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family 1.
 DR EMBL; BC065923; AAH65923.1; -
 DR HSBP; P20231; 1AOL.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:000508; F:proteolysis and peptidolysis; IEA.
 DR GO; GO:000508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1_
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_Spec; 1.
 DR PROSITE; PS00240; TRYP_SIN_DOM; 1.
 DR PROSITE; PS00134; TRYP_SIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYP_SIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 282 AA; 31296 MW; 9727DC527F9896CA CRC64;

Query Match 92.9%; Score 1405; DB 2; Length 282;
 Best Local Similarity 92.0%; Pred. No. 7.9e-114;
 Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSLILLALPVLASRAVAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMHFCG 60
 DB 8 MNLILLALPVLASRAVAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMHFCG 67
 QY 61 GSILHPQVLTAAHCGPVDKDLATLRVQLREOHLTYQDQLPVSRILVHPQFYIQTGA 120
 DB 68 GSILHPQVLTAAHCGPVDKDLATLRVQLREOHLTYQDQLPVSRILVHPQFYIQTGA 127
 QY 121 DIALLELEPPVNISSRVHTVTLPPASETFPPGMCWVGWDVNDDEPLPPFPPLKQYKV 180
 DB 128 DIALLELEPPVNISSRVHTVTLPPASETFPPGMCWVGWDVNDDEPLPPFPPLKQYKV 187
 QY 181 PIMENHICDAKYHGAATGYDDVRIIRDDMLCAGNSQSDCKDGGSLVCKVNGTWLQAG 240
 DB 188 PIMENHICDAKYHGAATGYDDVRIIRDDMLCAGNSQSDCKDGGSLVCKVNGTWLQAG 247
 QY 241 VVSWDEGCAQPNRPGIYTRVTVYLLDMIHIVPKKP 275
 DB 248 VVSWDEGCAQPNRPGIYTRVTVYLLDMIHIVPKKP 282

RESULT 8
 Q6FHB8 PRELIMINARY; PRT; 275 AA.

AC Q6FHB8;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE TP5B2 protein (Fragment).
 GN Name=TP5B2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Katzung K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zhu D., Hu Y., Labaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family 1.
 DR EMBL; CR541836; CAG46635.1; -
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:000508; F:proteolysis and peptidolysis; IEA.
 DR GO; GO:000508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1_
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_Spec; 1.
 DR PROSITE; PS00240; TRYP_SIN_DOM; 1.
 DR PROSITE; PS00134; TRYP_SIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYP_SIN_SER; 1.
 KW Hydrolyase; Protease; Serine protease.
 FT NON TER 275 AA; 30517 MW; ABD124C4293868BD CRC64;

Query Match 92.8%; Score 1403; DB 2; Length 275;
 Best Local Similarity 91.6%; Pred. No. 1.2e-113;
 Matches 252; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSLILLALPVLASRAVAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMHFCG 60
 DB 1 MNLILLALPVLASRAVAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMHFCG 60
 QY 61 GSILHPQVLTAAHCGPVDKDLATLRVQLREOHLTYQDQLPVSRILVHPQFYIQTGA 120
 DB 61 GSILHPQVLTAAHCGPVDKDLATLRVQLREOHLTYQDQLPVSRILVHPQFYIQTGA 120
 QY 121 DIALLELEPPVNISSRVHTVTLPPASETFPPGMCWVGWDVNDDEPLPPFPPLKQYKV 180
 DB 121 DIALLELEPPVNISSRVHTVTLPPASETFPPGMCWVGWDVNDDEPLPPFPPLKQYKV 180
 QY 181 PIMENHICDAKYHGAATGYDDVRIIRDDMLCAGNSQSDCKDGGSLVCKVNGTWLQAG 240
 DB 181 PIMENHICDAKYHGAATGYDDVRIIRDDMLCAGNSQSDCKDGGSLVCKVNGTWLQAG 240
 QY 241 VVSWDEGCAQPNRPGIYTRVTVYLLDMIHIVPKKP 275
 DB 241 VVSWDEGCAQPNRPGIYTRVTVYLLDMIHIVPKKP 275

RESULT 9
 Q6FHB8 PRELIMINARY; PRT; 275 AA.

AC Q6FHB8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Trypsin I.
 GN Name=trypsin;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21096910; PubMed=1157797; DOI=10.1093/hmg/10.4.339;
 RA Daniella R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
 RA Tharella C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT Mb of the short arm of human chromosome 16";
 RL Hum. Mol. Genet. 10:339-352(2001).
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL: AEO06466; AAK61271.1; -.
 DR HSSP: P20231; 1AOL.
 DR GO: GO:0004263; F:chymotrypsin activity; IEA.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0004295; F:trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR009003; Pept_Ser_Cys.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPsin.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00240; TRYPsin DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Hydroxylase; Protease; Serine protease.
 KW SEQUENCE 275 AA; 30601 MW; 2FAAAMAE7DDE483E CRC64;

Query Match 92.7%; Score 1401; DB 2; Length 275;
 Best Local Similarity 91.6%; Pred. No. 1.7e-113;
 Matches 252; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSLLILALPVLASRAVAAPAVQALQAGIVGGEAPRSKMPQVSLRVDRYMHFPG 60
 DB 1 MNLVLIALPVLASRAVAAPAVQALQAGIVGGEAPRSKMPQVSLRVDRYMHFPG 60
 QY 61 GSLLHPQWVLTAAHCLGPDVADLTLRVQLREOHLYYDDQLPVSRRIYHPOFYITQTA 120
 DB 61 GSLLHPQWVLTAAHCLGPDVADLTLRVQLREOHLYYDDQLPVSRRIYHPOFYITQTA 120
 QY 121 DIALLEBEPVNISSRVHTVMTLPPASETFPPGMPGVNDEBPLPPPPPLKQYKV 180
 DB 121 DIALLEBEPVNISSRVHTVMTLPPASETFPPGMPGVNDEBPLPPPPPLKQYKV 180
 QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQPSCKGDSGGLVCKVNGTWLQAG 240
 DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQPSCKGDSGGLVCKVNGTWLQAG 240
 QY 241 VVSWDEGCAQPNRPGLIYRTVYTLDMIHYYVKKP 275
 DB 241 VVSWDEGCAQPNRPGLIYRTVYTLDMIHYYVKKP 275
 RESULT 10
 QY 07YS62 PRELIMINARY; PRT; 275 AA.
 AC 07YS62;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Trypsin (EC 3.4.21.59).
 GN Name=mtcl;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Dacre K.J., McAliese S., Pemberton A., McGorum B.C.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Dacre K.J.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ515902; CAD56807.1; -.
 DR HSSP: P20231; 1AOL.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0004295; F:trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR009003; Pept_Ser_Cys.
 DR Pfam: PF00089; Trypsin; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00240; TRYPsin DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Hydroxylase; Protease; Serine protease.
 KW SEQUENCE 275 AA; 30476 MW; 718F574ADBE21ED CRC64;

Query Match 76.5%; Score 1156; DB 2; Length 275;
 Best Local Similarity 74.4%; Pred. No. 3.3e-92;
 Matches 203; Conservative 28; Mismatches 42; Indels 0; Gaps 0;

QY 1 MSLLILALPVLASRAVAAPAVQALQAGIVGGEAPRSKMPQVSLRVDRYMHFPG 60
 DB 1 MNLVLIALPVLASRAVAAPAVQALQAGIVGGEAPRSKMPQVSLRVDRYMHFPG 60
 QY 61 GSLLHPQWVLTAAHCLGPDVADLTLRVQLREOHLYYDDQLPVSRRIYHPOFYITQTA 120
 DB 61 GSLLHPQWVLTAAHCLGPDVADLTLRVQLREOHLYYDDQLPVSRRIYHPOFYITQTA 120
 QY 121 DIALLEBEPVNISSRVHTVMTLPPASETFPPGMPGVNDEBPLPPPPPLKQYKV 180
 DB 121 DIALLEBEPVNISSRVHTVMTLPPASETFPPGMPGVNDEBPLPPPPPLKQYKV 180
 QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQPSCKGDSGGLVCKVNGTWLQAG 240
 DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQPSCKGDSGGLVCKVNGTWLQAG 240
 QY 241 VVSWDEGCAQPNRPGLIYRTVYTLDMIHYYVKKP 273
 DB 241 VVSWDEGCAQPNRPGLIYRTVYTLDMIHYYVKKP 273
 RESULT 11
 MCT7_MOUSE
 ID MCT7_MOUSE STANDARD; PRT; 273 AA.
 AC 002844;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Mast cell protease 7 precursor (EC 3.4.21.55) (MMP-7) (tryptase).
 GN Name=Mcp7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2;
 RX MEDLINE=93087489; PubMed=1454796;
 RA McNeil H.P., Reynolds D.S., Schiller V., Childyal N., Gurley D.S.,
 RA Austen K.F., Stevens R.L.;
 RT "Isolation, characterization, and transcription of the gene encoding
 RT mouse mast cell protease 7.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11174-11178(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6J;
 RX MEDLINE=96162035; PubMed=8576265; DOI=10.1074/jbc.271.5.2851;
 RA Hunt J.E., Stevens R.L., Austen K.F., Zhang J., Xia Z., Childyal N.;
 RT "Natural disruption of the mouse mast cell protease 7 gene in the
 RT C57BL/6 mouse.";
 RL J. Biol. Chem. 271:2851-2855(1996).
 CC -1- FUNCTION: Trypsin is the major neutral protease present in mast
 cells and is secreted upon the coupled activation-degranulation

	CC	- response of this cell type.
	CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -, Lys- -, but
	CC	w/ich more restricted specificity than trypsin.
	CC	-1- ALTERNATIVE PRODUCTS:
	CC	Event=Alternative splicing; Named isoforms=2;
	CC	Comment=The alternative splicing event is due to a G to A point
	CC	muation at the exon 2/intron 2 splice site and causes loss of
	CC	protein expression. The alternatively spliced transcript is only
	CC	found in C57BL/6 mouse;
	CC	Name=1;
	CC	IsoId=Q02844-1; Sequence=Displayed;
	CC	Name=2; Synonyms=Truncated;
	CC	IsoId=Q02844-2; Sequence=VSP_005378, VSP_005379;
	CC	-1- DEVELOPMENTAL STAGE: Is not expressed in mature serosal or mucosal
	CC	mast cells and is expressed only transiently at an early stage of
	CC	in vitro mast cell differentiation.
	CC	-1- SIMILARITY: Belongs to the peptidase S1 family. Trypsase
	CC	subfamily.
	CC	-----
	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
	CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
	CC	the European Bioinformatics Institute. There are no restrictions on its
	CC	use by non-profit institutions as long as its content is in no way
	CC	modified and this statement is not removed. Usage by and for commercial
	CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/
	CC	or send an email to license@isb-sdb.ch).
	CC	-----
	DR	EMBL; L00654; AAA39993.1; -;
	DR	EMBL; L00653; AAA39992.1; -;
	DR	EMBL; U42405; AAA97874.1; -;
	DR	EMBL; U42406; AAA97875.1; -;
	DR	PIR; A47246; A47246.
	DR	HSSP; P15157; ILTO.
	DR	MEROPS; S01.026; --
	DR	MGD; MGI:96943; Mcrpl7.
	DR	InterPro; IPR009003; Pept Ser Cys.
	DR	InterPro; IPR001254; Peptidease_S1.
	DR	InterPro; IPR001314; Peptidease_S1A.
	DR	Pfam; PF00089; Trypsin; 1.
	DR	PRINTS; PR00722; CHYMOTRYPSIN.
	DR	SMART; SMO0020; Tryp_SPE; 1.
	DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
	DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
	DR	PROSITE; PS00135; TRYPSIN_SER; 1.
	KW	Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
	KM	Signal; Zymogen.
	FT	SIGNAL 1 18 potential.
	FT	PROPEP 19 28 Activation peptide (Potential).
	FT	CHAIN 29 273 Mast cell protease 7.
	FT	ACT_SITE 72 73 Charge relay system (By similarity).
	FT	ACT_SITE 119 119 Charge relay system (By similarity).
	FT	ACT_SITE 222 222 Charge relay system (By similarity).
	FT	DISULFID 57 73 Charge relay system (By similarity).
	FT	DISULFID 153 228 By similarity.
	FT	DISULFID 186 209 By similarity.
	FT	CABOHYD 49 49 N-linked (GlcNAc...) (Potential).
	FT	CABOHYD 130 130 N-linked (GlcNAc...) (Potential).
	FT	VASPLIC 44 46 VSL->GCC (in isoform 2).
	FT	VASPLIC 47 273 /FTId=VSP_005378.
	FT	VARSPPLIC 47 273 Missing (in isoform 2).
	FT	/FTId=VSP_005379.
	SO	SEQUENCE 273 AA; 30337 MW; 50ECBA765294205E CRC64;
		Query Match 75.0%; Score 1134; DB 1; Length 273;
		Best Local Similarity 74.4%; Pred. No. 2.7e-90;
		Matches 203; Conservative 23; Mismatches 45; Indels 2; Gaps 1;
Oy		1 MLSTLLTLPLVLASRAVAAPAVQALQQAGIVGGGEAPRSKMPQVSILVRDRYMMHFCG 60
		: : : : : : : : : : : : : : : : :
Dd		1 MKULLLTLPILLSLVHAAPG--AMTRREGIVGCGEAIQNKPKMPQVSLRANDTYMMHFCG 58
Oy		61 GSLHPQAVLTAAHCLGPVDVKLATLRVQLREQHLYYDDQLIPVSRITVHPQFYIIQTGA 120

Dc		59	GSLIHQWLTAAHCVGVDADPNKVRVQLAKQYLYNHDLMWTYSQIITHPDFITVGDA	118
Qy		121	DIALEELEPNISSRVHTTWM.LPPASEFPFGMPCWTGKDUNDDELPPLPFLLKOVKY	186
Dc		119	DIALTLTPNPVISDVHPVLPEPASEFEPGGTLCTWTGMGININGVNLPPLPFLLKEVOY	178
Qy		181	PIMENHICDAXHGLAAYNGDDRIIRIDMLCAGNSQSDSCSGDSGGLVCYNSTMLQAG	246
Dc		179	PIIEHLCSOLKHKKGLITGDNVHYTRDMLCAGBEGHDSCGDSGGPLVCXVEDPTLLOAG	238
Qy		241	VVSMDGCAQPNNRPGIYRTRYTYLDMMHHYYPK	273
Dc		239	VVSMGBCAQPNRPGLIYTRYTYLDMMHHYYPK	271
<hr/>				
RESULT 12				
MCT6	MOUSE			
ID	_MCT6_MOUSE	STANDARD;	PRT;	276 AA.
AC	P21845,	O61962;		
DT	01-MAY-1991	(Rel. 18,	Created)	
DT	01-AUG-1991	(Rel. 19,	Last sequence update)	
DT	25-OCT-2004	(Rel. 45,	Last annotation update)	
DE	Mast cell protease 6 precursor (EC 3.4.21.59) (MMC6P-6) (Trypsin).			
OS	Name=MCT6;			
OC	Mus musculus (Mouse).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCB1_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RK	MEDLINE=91139682; PubMed=1995638;			
RA	Raynolds D.S., Gurley D.S., Austen K.F., Serafin W.E.;			
RT	"Cloning of the cDNA and gene of mouse mast cell protease-6.			
RT	Transcription by progenitor mast cells and mast cells of the			
RL	connective tissue subclass."			
J. Biol. Chem.	266:3847-3853(1991).			
[2]				
RP	SEQUENCE FROM N.A.			
RC	STRATIN=Leaden X AI;			
RX	MEDLINE=94023807; PubMed=8210998;			
RA	Huang R., Abrik M., Gohl A.E., Nilsson G., Aveskogh M., Larsson L.G.,			
RT	Nilsson K., Hellman U.;			
RT	"Expression of a mast cell tryptase in the human monocytic cell lines			
U-937 and Mono Mac 6.";				
Scand. J. Immunol.	38:359-367(1993).			
[3]				
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RC	STRATIN=Leaden X AI;			
RX	MEDLINE=95048582; PubMed=7959952;			
RA	Huang R., Hellman L.T.;			
RT	"Gene for mast-cell serine protease and their molecular evolution.";			
Immunogenetics	40:397-414(1994).			
[4]				
RP	SEQUENCE FROM N.A. (ISOFORM LONG).			
RC	STRATIN=FVB/N; TISSUE=Colon;			
RX	MEDLINE=22338827; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Deane J.G.,			
Altauer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
Alecshul S.P., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,				
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien P.,				
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,				
Brownstein M.J., Usdin T.B., Toshynki S., Carninci P., Prange C.,				
Raba S.S., Loggellano N.A., Peters G.J., Abrahamson R.D., Mullaly S.J.,				
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarone P.H.,				
Villarado S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huily S.W.,				
Killeen D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
Fahney J., Helton B., Ketteman M., Madan A., Rodriguez S., Sanchez A.,				
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,				
Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,				
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,				

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [5].
 RX MEDLINE=90222202; PubMed=2326280;
 RA Reynolds D.S., Stevens R.L., Lane W.S., Carr M.H., Austen K.F.,
 RA Seratin W.E.;
 RT "different mouse mast cell populations express various combinations of
 RT at least six distinct mast cell serine proteases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3230-3234(1990).
 CC -1- FUNCTION: Trypsin is the major neutral protease present in mast
 CC cells and is secreted upon the coupled activation-degranulation
 CC response of this cell type.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|- , Lys-|- , but
 CC with more restricted specificity than trypsin.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P21845-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P21845-2; Sequence=VSP_005376; VSP_005377;
 CC Note=probably non functional.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Trypsin
 CC subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M57625; AAA39988.1; -;
 DR EMBL; M57625; AAA39987.1; -;
 DR EMBL; L31853; AAA39725.1; -;
 DR EMBL; X78542; CAA55288.1; -;
 DR EMBL; BC024374; AAH24374.1; -;
 DR PIR; A38654; A38654.
 DR PIR; I48685; I48685.
 DR HSSP; P20231; 1A0L.
 DR MEROPS; S01.025; -;
 DR WGD; MGI:96542; Mcp6.
 DR GO; GO:0008201; F:heparin binding; IDA.
 DR GO; GO:000515; F:protein binding; IPI.
 DR GO; GO:0030019; F:trypsin activity; IDA.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP SPc; 1.
 DR PROSITE; PS00240; TRYPSPIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSPIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSPIN_SER; 1.
 KW Alternative splicing; Direct protein sequencing; Glycoprotein;
 KW Hydrolyase; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 21
 FT PROPEP 22 31
 FT CHAIN 32 276
 FT ACT_SITE 75 75
 FT ACT_SITE 122 122
 FT ACT_SITE 225 225
 FT DISULFID 60 76
 FT DISULFID 156 231
 FT DISULFID 189 212
 FT DISULFID 221 249
 FT CARBOHYD 133 133
 FT VARSPDIC 223 230
 FT VARSPDIC 231 276
 FT VARSPDIC 231 276

FT SEQUENCE 276 AA; 30927 MW; 525B2C9A04A72200 CRC64;
 SQ
 Query Match 74.9%; Score 1133; DB 1; Length 276;
 Best Local Similarity 73.3%; Pred. No. 3.3e-90;
 Matches 198; Conservative 28; Mismatches 42; Indels 2; Gaps 1;
 QY 4 LILLALPVLASRAVAAPPAVALQAGIVGGQAEPRSRMPQVSLRVRDRITWAFRCGSL 63
 DB 7 LILMALSLIASLIVSAPRP--ANCRVIGVGHSEASESRKMPQVSLRFLNTNWIHFCGSL 64
 QY 64 IHPQVNLTAARHGLGPDVNDLTLRYQREOHLYYQDQLPVSRIIVHPOFTIQQGADIA 123
 DB 65 IHPQVNLTAARHGVGHISPOLFRVQLREQYLYGDDQLSLRVLVHPHTTAEGADVA 124
 QY 124 LLELEPVNVSSRVTWMLPPASRTFPPGMPGCVTGMGDVNDDEPLPPFPKQKVPIM 183
 DB 125 LLELEPVNVSTHHPISLPASRTFPPGTSQWVVGWGDINDDEPLPPFPKQKVPIM 184
 QY 184 ENHICDARKYHGLGATYGDVRIIRDMLCAQNSQSDSCGSGPLVCKVNTWLAQVVS 243
 DB 185 ENSLCDRKXHTGLYGDVDFPIVHDGMLCAGNTRRDSGSGSGPLVCKVNTWLAQVVS 244
 QY 244 WDEGCAQPNRPGIYRTVYTLDMTHYVPK 273
 DB 245 WDEGCAQPNRPGIYRTVYTLDMTHYVPK 274
 QY
 DB
 RESULT 13
 TRYT CANFA
 ID TRYT CANFA STANDARD; PRT; 275 AA.
 AC P15944;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Trypsin precursor (BC 3.4.21.59).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 ON NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352460; PubMed=2504277;
 RA Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
 RT "Molecular cloning of dog mast cell trypsin and a related protease:
 RT structural evidence of a unique mode of serine protease activation.";
 RL Biochemistry 28:4148-4155(1989).
 CC -1- FUNCTION: Trypsin is the major neutral protease present in mast
 CC cells and is secreted upon the coupled activation-degranulation
 CC response of this cell type.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|- , Lys-|- , but
 CC with more restricted specificity than trypsin.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Released from the secretory granules upon
 CC mast cell activation.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Trypsin
 CC subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration -
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M24664; AAA30854.1; -;
 DR PIR; A32410; A32410.
 DR HSSP; P20231; 1A0L.
 DR MEROPS; S01.118; -;
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR

DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Glycoprotein; Hydrolase; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 20 Potential.
 FT PROPEP 1 30 Activation peptide (By similarity).
 FT CHAIN 31 275 Trypsase.
 FT ACT_SITE 74 74 Charge relay system (By similarity).
 FT ACT_SITE 121 121 Charge relay system (By similarity).
 FT ACT_SITE 224 224 Charge relay system (By similarity).
 FT DISULFID 59 75 By similarity.
 FT DISULFID 155 230 By similarity.
 FT DISULFID 188 211 By similarity.
 FT DISULFID 220 248 By similarity.
 FT CAROXYD 132 132 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 275 AA; 30088 MW; C38869251F248D5B CRC64;
 Query Match 74.8%; Score 1131; DB 1; Length 275;
 Best Local Similarity 72.7%; Pred. No. 4,9e-90;
 Matches 200; Conservative 30; Mismatches 45; Indels 0; Gaps 0;
 QY 1 MSLLLLALPVLASRAVAPVQALQAGIGVGOEAPRSKPMQVSLVRDRYMMHPCG 60
 DB 1 MSPPLVLAALGSLVPSVAPQALQKRGIVGSRAPSKPMQVSLKQYWRHICG 60
 QY 61 GSLIHPQWVLAACIGPVDVADLTIRVQAREQHLVYQDQLPVSRILVHPQFYIIQTGA 120
 DB 61 GSLIHPQWVLAACIGPVDVADLTIRVQAREQHLVYQDQLPVSRILVHPQFYIIQTGA 120
 QY 121 DIALLELEPNISSRVATWMLPPASETFPPGMPGCVTGMVDNDEPLPPFPPLKQYKV 180
 DB 121 DIALLELEPNISSRVATWMLPPASETFPPGMPGCVTGMVDNDEPLPPFPPLKQYKV 180
 QY 121 DIALLELEPNISSRVATWMLPPASETFPPGMPGCVTGMVDNDEPLPPFPPLKQYKV 180
 DB 121 DIALLELEPNISSRVATWMLPPASETFPPGMPGCVTGMVDNDEPLPPFPPLKQYKV 180
 QY 181 PIMENHICDAHYHAGYGDVRIIRDDMLCAGNSQSDSCGDSGGLVCKVNGTMDLQAG 240
 DB 181 PIMENHICDAHYHAGYGDVRIIRDDMLCAGNSQSDSCGDSGGLVCKVNGTMDLQAG 240
 QY 241 VVSWDEGCAQPNRPGLYTRVTVYLDWIMHHYVPK 275
 DB 241 VVSWDEGCAQPNRPGLYTRVTVYLDWIMHHYVPK 275
 QY 241 VVSWDEGCAQPNRPGLYTRVTVYLDWIMHHYVPK 275
 DB 241 VVSWDEGCAQPNRPGLYTRVTVYLDWIMHHYVPK 275
 RESULT 14
 Q92IN4 PRELIMINARY; PRT; 273 AA.
 AC Q92IN4
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Mast cell protease 7.
 GN Name=Mcp7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappelen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Franke C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fabry J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skala U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -i- SIMILARITY: belongs to peptidase family S1.
 DR EMBL; BC011328; AAH11328.1; -.
 DR HSSP; P15157; ILTO.
 DR MGD; MGI:96943; Mcp7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 273 AA; 30332 MW; 51417476514035BE CRC64;
 Query Match 74.3%; Score 1123; DB 2; Length 273;
 Best Local Similarity 74.0%; Pred. No. 2,4e-89;
 Matches 202; Conservative 22; Mismatches 47; Indels 2; Gaps 1;
 QY 1 MSLLLLALPVLASRAVAPVQALQAGIGVGOEAPRSKPMQVSLVRDRYMMHPCG 60
 DB 1 MSLLLLALPVLASRAVAPVQALQAGIGVGOEAPRSKPMQVSLVRDRYMMHPCG 60
 QY 61 GSLIHPQWVLAACIGPVDVADLTIRVQAREQHLVYQDQLPVSRILVHPQFYIIQTGA 120
 DB 61 GSLIHPQWVLAACIGPVDVADLTIRVQAREQHLVYQDQLPVSRILVHPQFYIIQTGA 120
 QY 121 DIALLELEPNISSRVATWMLPPASETFPPGMPGCVTGMVDNDEPLPPFPPLKQYKV 180
 DB 121 DIALLELEPNISSRVATWMLPPASETFPPGMPGCVTGMVDNDEPLPPFPPLKQYKV 180
 QY 121 DIALLELEPNISSRVATWMLPPASETFPPGMPGCVTGMVDNDEPLPPFPPLKQYKV 180
 DB 121 DIALLELEPNISSRVATWMLPPASETFPPGMPGCVTGMVDNDEPLPPFPPLKQYKV 180
 QY 181 PIMENHICDAHYHAGYGDVRIIRDDMLCAGNSQSDSCGDSGGLVCKVNGTMDLQAG 240
 DB 181 PIMENHICDAHYHAGYGDVRIIRDDMLCAGNSQSDSCGDSGGLVCKVNGTMDLQAG 240
 QY 241 VVSWDEGCAQPNRPGLYTRVTVYLDWIMHHYVPK 273
 DB 241 VVSWDEGCAQPNRPGLYTRVTVYLDWIMHHYVPK 273
 QY 241 VVSWDEGCAQPNRPGLYTRVTVYLDWIMHHYVPK 273
 DB 241 VVSWDEGCAQPNRPGLYTRVTVYLDWIMHHYVPK 273
 RESULT 15
 Q96RZ7 PRELIMINARY; PRT; 233 AA.
 AC Q96RZ7
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Mast cell tryptase beta III.
 GN Name=tryptaseb;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21096910; PubMed=1157797; DOI=10.1093/mmg/10.4.339;
 RA Daniels R.J., Peden J.F., Lloyd C., Horeley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2

RT Mb of the short arm of human chromosome 16.;
RL Hum. Mol. Genet. 10:339-352(2001).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL: AE006466; AAK61270.1; -.
DR HSSP: P20231; 1A0L.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase S1.
DR InterPro: IPR001314; Peptidase S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 233 AA; 25874 MW; 246A96C71B2CE6D0 CRC64;

Query Match 74.1%; Score 1120; DB 2; Length 233;

Best local Similarity 92.3%; Pred. No. 3,7e-89;
Matches 204; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSLLLALPVLASRAVAPAPVQALQAGIVGGGEAPRSKMPQVSLRVRDRYWMHFCG 60
DB 1 MNLILLALPVLASRAVAPAPVQALQAGIVGGGEAPRSKMPQVSLRVRDRYWMHFCG 60
QY 61 GSLIHPOWLTAAHCGPDVYKDLATLRVQLREOHLVYQDQLPVSRIIVHPOFYIIQTGA 120
DB 61 GSLIHPOWLTAAHCGPDVYKDLATLRVQLREOHLVYQDQLPVSRIIVHPOFYIIQTGA 120
QY 121 DIALLELEBPVNISRVHTVMLPPASETPPGMPCWVTGNGVDVNDDEPLPPPEPLKQVKV 180
DB 121 DIALLELEBPVNISRVHTVMLPPASETPPGMPCWVTGNGVDVNDDEPLPPPEPLKQVKV 180
QY 181 PIMENHICDAKHLGAYTGDDVRIIRDMLCAGNSORDSCK 221
DB 181 PIMENHICDAKHLGAYTGDDVRIIRDMLCAGNTRRDSCK 221

Search completed: August 27, 2005, 23:29:07
Job time : 133 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 27, 2005, 23:39:06 ; Search time 615 Seconds

(without alignments)
2925.772 Million cell updates/sec

Title: US-09-598-982C-52

Perfect score: 1512

Sequence: 1 MSLTLLALPVLASRAVAP.....ITYRTYTLDMIHVPPKP 275

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 7331713 seqs, 327154945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1p
-O=/cgn2_1/USPTO.spool.p/US09598982/rnatc.25082005.165827.1602/app.query.fasta_1.455
-DB=Published Applications NA -QMT=faetrap -SUPFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNIT5=bits -START=1 -END=1 -MATRIX=DIAGONAL62
-FRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09598982 @CGN 1.1 723 @rnatc.25082005.165827.1602
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10J_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11A_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	1512	100.0	1154	17	US-10-352-684A-45	Sequence 45, Appl
2	1512	100.0	1158	14	US-10-116-802-240	Sequence 240, App
3	1512	100.0	1158	21	US-10-956-157-1042	Sequence 1042, Ap
4	1416	93.7	1334	20	US-10-723-860-6799	Sequence 6799, Ap
5	1414	93.5	828	18	US-10-287-226-89	Sequence 89, Appl
6	1411	93.3	828	18	US-10-287-226-91	Sequence 91, Appl
7	1411	93.3	1193	17	US-10-956-157-1043	Sequence 1043, Ap
8	1405	92.9	1143	17	US-10-352-684A-47	Sequence 47, Appl
9	1405	92.9	1145	18	US-10-287-226-93	Sequence 93, Appl
10	1405	92.9	1148	18	US-10-956-157-2444	Sequence 2444, Ap
11	1401	92.7	2662	18	US-10-275-505-27	Sequence 27, Appl
12	1394	92.2	1081	9	US-09-954-456-2126	Sequence 2126, Ap
13	1394	92.2	1081	10	US-09-960-706-680	Sequence 680, App
14	1394	92.2	1081	10	US-09-873-319-427	Sequence 427, App
15	1394	92.2	1081	10	US-09-873-367C-155	Sequence 155, App
16	1394	92.2	1081	10	US-09-873-367C-714	Sequence 714, App
17	1394	92.2	1081	21	US-10-843-641A-155	Sequence 155, App
18	1394	92.2	1081	21	US-10-843-641A-714	Sequence 714, App
19	1394	92.2	1081	21	US-10-843-641A-5153	Sequence 5153, Ap
20	1356.5	89.7	858	18	US-10-287-226-87	Sequence 87, Appl
21	1246.5	82.4	5456	22	US-10-723-860-2689	Sequence 2689, Ap
22	1246.5	82.4	5456	22	US-10-756-149-2484	Sequence 2484, Ap
23	1134	75.0	1187	18	US-10-275-505-22	Sequence 22, Appl
24	1108	73.3	729	21	US-10-480-988-55	Sequence 55, Appl
25	1100	72.8	729	21	US-10-956-157-1789	Sequence 1789, Ap
26	953	63.0	600	21	US-10-956-157-7024	Sequence 7024, Ap
27	687.5	45.5	846	10	US-09-813-432-11	Sequence 11, Appl
28	687.5	45.5	846	17	US-10-174-364-11	Sequence 11, Appl
29	687.5	45.5	846	18	US-10-246-583-11	Sequence 11, Appl
30	687.5	45.5	846	19	US-10-689-832-11	Sequence 11, Appl
31	643	42.5	873	14	US-10-117-323-2	Sequence 2, Appl
32	632.5	41.8	1199	21	US-10-956-157-1816	Sequence 1816, Ap
33	616	40.7	825	14	US-10-117-323-1	Sequence 1, Appl
34	606.5	40.1	948	16	US-10-131-409-15	Sequence 15, Appl
35	606.5	40.1	948	17	US-10-139-854-15	Sequence 15, Appl
36	606.5	40.1	948	17	US-10-150-813-15	Sequence 15, Appl
37	606.5	40.1	948	17	US-10-150-811-15	Sequence 15, Appl
38	604.5	40.0	1958	17	US-10-311-035-29	Sequence 29, Appl
39	603.5	39.9	1122	9	US-09-900-754-1	Sequence 1, Appl
40	601	39.7	858	16	US-10-131-409-21	Sequence 21, Appl
41	601	39.7	858	17	US-10-139-854-21	Sequence 21, Appl
42	601	39.7	858	17	US-10-150-813-21	Sequence 21, Appl
43	601	39.7	858	17	US-10-150-811-21	Sequence 21, Appl
44	588	38.9	383	10	US-09-918-595-6378	Sequence 6378, Ap
45	587.5	38.9	870	16	US-10-131-409-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-352-684A-45
; Sequence 45, Application US/10352684A
; Publication No. US20030215552A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12203, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MP102-019P1RNONMIM

```

CURRENT APPLICATION NUMBER: US/10/352,684A
CURRENT FILING DATE: 2003-01-28
PRIORITY APPLICATION NUMBER: US 60/354,333
PRIORITY FILING DATE: 2002-02-04
PRIORITY APPLICATION NUMBER: US 60/360,258
PRIORITY FILING DATE: 2002-02-28
PRIORITY APPLICATION NUMBER: US 60/364,476
PRIORITY FILING DATE: 2002-03-15
PRIORITY APPLICATION NUMBER: US 60/375,626
PRIORITY FILING DATE: 2002-04-26
PRIORITY APPLICATION NUMBER: US 60/386,494
PRIORITY FILING DATE: 2002-06-06
PRIORITY APPLICATION NUMBER: US 60/390,965
PRIORITY FILING DATE: 2002-06-24
PRIORITY APPLICATION NUMBER: US 60/392,480
PRIORITY FILING DATE: 2002-06-28
PRIORITY APPLICATION NUMBER: US 60/394,128
PRIORITY FILING DATE: 2002-07-03
PRIORITY APPLICATION NUMBER: US 60/399,783
PRIORITY FILING DATE: 2002-07-31
PRIORITY APPLICATION NUMBER: US 60/403,221
PRIORITY FILING DATE: 2002-08-13
Removing Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FaSTSeq For Windows Version 4.0
SEQ ID NO 45
LENGTH: 1154
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (18) ... (845)
US-10-352-684A-45

```

Alignment Scores:	
Pred. No.:	5,51e-171
Score:	1512.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	17
US-09-598-982C-52 (1-275) × US-10-352-684A-45 (1-1154)	
	length: 1154
	Matches: 275
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

QY	1	MetLeuSerLeuLeuLeuLeuLeuLeuProValLeuAlaSerArgAlaATyAlaAlaPro	20
Db	18	ATCTAGAGCTGCTGCTGCTGGAGCGCTCCGCTCTGGAGAGCCGGGCTTAGCGAGCCCTT	77
QY	21	AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlnGlnAlaProArgSer	40
Db	78	GCCCCAGTCCAGGCCCTTGCAGAGAGGGATATCTGTGGGGGATCGAGAGGCCCCCAAGAGC	137
QY	41	LeuTyrProTyrGlnValSerLeuArgValAlaArgAspArgTyrTyrMetHisPheCysGly	60
Db	138	AAATGGAGCCCTGGAGAGGTGAGCTGAGAGTCCCGAGCCGATACTGATGACATTTCGGCGG	197
QY	61	GlySerLeuIleHisProGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspVal	80
Db	198	GGCTCCCTCATCAACCCCGAGTGGGTGCTGACCGGGGGGCACTGCTGGAGCCGAGCTC	255
QY	81	LeuAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGln	100
Db	258	AAAGATCTGGCCACCTCTAGGGGTGACACTGGGGAGAGCAAGCACTTACTACAGAGACAG	317
QY	101	LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla	120
Db	318	CTGCTGCAGTACGACGAGATCATCTGGACCCACAGTTCTATCATATGCAACCTGGAGCG	377
QY	121	AspIleAlaLeuLeuGlnLeuGlnGlnProValAsnIleSerSerArgValHisThrVal	140
Db	378	GATATCGCCCTGTGTGAGGTGGAGGAGCCCGTGAACATCTCCAGGCCGGGTCCACAGGTC	437
QY	141	MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTyrValIleHisTyr	160

Db	438	ATGCTGCCCCCTGCTCGAGAGACTTTCCCCCGGGAGATGCCGTGCTGGGTCACTGGGTGG	497
OY	161	G1yAspVal1AspAsnAspGluProLeuProProPheProLeuValysVal	180
Db	498	GGGAGTGTGACAAATGATGAGCCCTCCACCGGCATTCCCCCGAAGCAGGGAAGTTC	557
OY	181	Pro11MetG1uAsnHis11IeCyAspAsp1a1ysrTrh1sleuG1yAla1yTrhTrhG1yAsp	200
Db	558	CCCATTAATGAAAACCAACATTGTTGTACCCAAAATACCACTTGGCGGCTTACACGGAGAC	617
OY	201	AspVal1Arg1e11eArgAspAspMetLeuCyAsp1aG1yAsnSerG1nArgAspSerCyS	220
Db	618	GAGTCCGATATCCGTGACGACATGCTGTGTCCGGAAACAGCCAGAGGACCTCTGC	677
OY	221	LySG1yAspSerG1yG1yProleuVal1ysetrVal1AsnG1yTrhTr1PleuG1nAlaG1y	240
Db	678	AAAGGGGACCTCGAGAGGGCCCTGGTGTGCAAGGTAATGGCACTGGCTACAGGCGGGC	737
OY	241	Val1aSerTr1PAspGluG1yCyAsp1aG1nProAsnArgProG1y11e1yTrhArgVal	260
Db	738	GTGGTCAGCTGGGAGCAGAGGCGTGTGCCACAGCCAAACCGGCTGGCATCTACACCGGTTC	797
OY	261	ThrTr1yTr1LeuAspTr11eHis1His1yTr1a1Pro1y1s1yPro	275
Db	798	ACCTACTACTGGACTGAGTCCACACATATGTCCCCAAAAGCCG	842

```

US-10-116-802-240
US-RESULT 240
Sequence 240, Application US/10116802
Publication No. US20030065157A1
GENERAL INFORMATION:
APPLICANT: Amy Lassek
TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
FILE REFERENCE: PA-0045 US
CURRENT APPLICATION NUMBER: US/10/116, 802
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/281,593
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 519
SOFTWARE: PERL Program
SEQ ID NO 240
LENGTH: 1158
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 378633.40
US-10-116-802-240

```

Alignment Scores:	
Pred. No.:	5.54e-171
Score:	1512.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	14

US-09-5598-982C-52 (1-275) x US-10-116-802-240 (1-1158)

Qy	1	MettLeuSerLeuIleuHeuLeuAlaLeuProValLeuAlaSerArgAlaIyrIrrAlaAlaPro	20
Db	18	ATGTGTAGCCTGTGTGTGTGTGGCGCGCCCGTCTGTGGCAGCGCGCGCTTAACCGCGCCCT	777
Qy	21	AlaProValAlaGlnAlaLeuGlnGlnAlaIaGlyIleValaGlyGlnGlnIuAlaProArgSer	40
Db	78	GCCCCAAGTCCAGGCGCCTGCAGCAGAAGCGGGATATGTGTGGGGAGTCAAGAGGCCCCCAAGAAC	13
Qy	41	LyseIrrProTrpGlnValSerLeuAArgValArgAspArgTyrTrpMetHisPheCysGly	60
Db	138	AAAGTGCGCCTGGCAGGTGAAGCTCGAAGATCCGGAGCCGATTACTGATGACACTTTCGGGG	19
Qy	61	GlySerLeuIleHisProGlnIrrProValLeuThrAlaAlaHisCysLeuGlyProAspVal	80

```
|||||
Db 198 GGCCTCCCTCATCCACCCCAAGTGGGAGTGCACCGGGGGGCACTGCTGGAGACGGAGCGTC 257
Qy 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTrpGlnAspGln 100
Db 258 AAGGATCTGGCCACCTCTCGGGGTGCACACGCGGAGCAGCACCTTACTACCAAGAGCAG 317
Qy 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120
Db 318 CTGCTGCCAGTCAGACGAGATCATCTGTGCACCCACAGTTTCTACATCATCCAGCTGAGCG 377
Qy 121 AspIleAlaLeuLeuGlnLeuGlnGlnProValAsnIleSerSerArgValHisThrVal 140
Db 378 GATATCGCCCTCTGGAGCTGGAGGAGCCGTAACATCTCCAGCGGGTCCACACGGCTC 437
Qy 141 MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTrpValThrGlyTrp 160
Db 438 ATGCTGCCCCCTGCTCGGAGACCTTCCCCCGGGGATGCTCGTGGGTCACTGGCTGG 497
Qy 161 GlyAspValAspAsnAspGlnProLeuProProProPheProLeuGlnValIleVal 180
Db 498 GCGCATGTGGACAATGATAGCCCTCCACCGCAATTTCCCTGAAGCAGGTGAAGGTC 557
Qy 181 ProIleMetGluAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
Db 558 CCCATTAATGGAAACACACATTTGTGACGCAAAATACACCTTGGCGCCCTACACGGGAGAC 617
Qy 201 AspValArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
Db 618 GACGTCCGCAATCATCCGTACGACATGCTGTGCGCGGAAACAGCAGAGGAGCATCTGTC 677
Qy 221 LysGlyAspSerGlnGlyProLeuValCysIleValAsnGlyThrTrpLeuGlnIleGly 240
Db 678 AAGGCGCACTGTGAGGGGCCCTGTGTGTGCAAGGTGAATGGCACTGTGCTACAGCGGGC 737
Qy 241 ValValSerTrpAspGlnGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgVal 260
Db 738 GTGTGACGTGGAGCAGAGGGCTGTGCGCAGCCCAACGGGCTGGCATCTACACCGGTGTC 797
Qy 261 ThrTyrTyrLeuAspTrpIleHisIleTyrValProIleValPro 275
Db 798 ACCTACTACTGTGACTGATCCACACATATGTCTCCCAAAAAGCCG 842

RESULT 3
US-10-956-157-1042
; Sequence 1042, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1042
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-1042

Alignment Scores:
Pred. No.: 5,54e-171 Length: 1158
Score: 1512.00 Matches: 275
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-598-982C-52 (1-275) x US-10-956-157-1042 (1-1158)
```

```
Qy 1 MetLeuSerLeuLeuLeuAlaLeuProValIleuAlaSerArgAlaTyrAlaAlaPro 20
Db 18 ATGCTGAGCCCTGCTGCTGCTGCGCTGCGCTGCTGCGAGACCGCGCTTACAGCGGCCCT 77
Qy 21 AlaProValGlnAlaLeuGlnGlnIleGlyIleValGlyGlnGlnAlaProArgSer 40
Db 78 GCCCCAGTCACAGGCCCTGACAGCAAGCGGGTATCTCGGGGGTCAAGAGGCCCCCAAGAGC 137
Qy 41 LysTrpProTrpGlnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGly 60
Db 138 AAGTGGCCCTGGCAGGTGAGCTTGAAGTCCGCAACGATATCTGATGACATTTCTGGGG 197
Qy 61 GlySerLeuIleHisProGlnTrpValLeuThrAlaHisCysLeuGlyProAspVal 80
Db 198 GGCCTCCCTCATCCACCCCACTGGGTGTGACCGCGGCGCATCTGCTGGAGCCGGAAGTTC 257
Qy 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTrpGlnAspGln 100
Db 258 AAGGATCTGGCCACCTCTCAGGGTGCACCTGGGAGAGCAGACCTTACTACCAAGAGCAG 317
Qy 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120
Db 318 CTGCTGCCAGTCAGACGAGATCATCTGTGCACCCACAGTTTCTACATCATCCAGCTGAGCG 377
Qy 121 AspIleAlaLeuLeuGlnLeuGlnGlnProValAsnIleSerSerArgValHisThrVal 140
Db 378 GATATCGCCCTCTGGAGCTGGAGGAGCCCGTAACATCTCCAGCGGGTCCACACGGCTC 437
Qy 141 MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTrpValThrGlyTrp 160
Db 438 ATGCTGCCCCCTGCTCGGAGACCTTCCCCCGGGGATGCTCGTGGGTCACTGGCTGG 497
Qy 161 GlyAspValAspAsnAspGlnProLeuProProProPheProLeuGlnValIleVal 180
Db 498 GCGCATGTGGACAATGATAGAGCCCTCCACCGCAATTTCCCTGAAGCAGGTGAAGGTC 557
Qy 181 ProIleMetGluAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
Db 558 CCCATTAATGGAAACACACATTTGTGACGCAAAATACACCTTGGCGCCCTACACGGGAGAC 617
Qy 201 AspValArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
Db 618 GACGTCCGCAATCATCCGTACGACATGCTGTGCGCGGAAACAGCAGAGGAGCATCTGTC 677
Qy 221 LysGlyAspSerGlnGlyProLeuValCysIleValAsnGlyThrTrpLeuGlnIleGly 240
Db 678 AAGGCGCACTGTGAGGGGCCCTGTGTGTGCAAGGTGAATGGCACCTGTGCTACAGCGGGC 737
Qy 241 ValValSerTrpAspGlnGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgVal 260
Db 738 GTGTGACGTGGAGCAGAGGGCTGTGCGCAGCCCAACGGGCTGGCATCTACACCGGTGTC 797
Qy 261 ThrTyrTyrLeuAspTrpIleHisIleTyrValProIleValPro 275
Db 798 ACCTACTACTGTGACTGATCCACACATATGTCTCCCAAAAAGCCG 842

RESULT 4
US-10-723-860-6799
; Sequence 6799, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsaeha
; APPLICANT: Ginsburg, Wendy M.
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882,0193, US08/1
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
```

/ SEQ ID NO 6799
/ LENGTH: 1334
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-723-860-6799

Alignment Scores:
Pred. No.: 2,23e-159 Length: 1334
Score: 1416.00 Matches: 255
Percent Similarity: 95.64% Conservative: 8
Best Local Similarity: 92.73% Mismatches: 12
Query Match: 93.65% Indels: 0
DB: 20 Gaps: 0

US-09-598-982c-52 (1-275) x US-10-723-860-6799 (1-1334)

```
QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaAlaPro 20
DB 53 ATGCTGAATCTGTGCTGTGGCGCTGCCGTCTGGCGAGCGCGCTTACCGCGCCCT 112
QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlyGlnGlnAlaProArgSer 40
DB 113 GCGCCAGCGCGAGCGCGCTGCGAGCGAGTGGGCGATCGTGGGGGTGAGAGCGCGCGAGAGC 172
QY 41 LysTrpProTrpGlnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGly 60
DB 173 AAGTGGCGCTGGCAGGTGAGCTGAGAGTCCGCGGCCACTGATGACCTTCTCGCGG 232
QY 61 GlySerLeuLeuLeuHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
DB 233 GGGTCCCTCATTCACACCCCGAGGGGTGCTGACCGAGCGAGCTGCGGAGCGAGCGT 292
QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTrpGlnAspGln 100
DB 293 AAGGATCTGGCGCGCGCTGAGGGTGCACACTGCGGAGACAGACCTCTTACACAGACAG 352
QY 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120
DB 353 CTGCTCGCGGTGACAGGATCATCTGACACCCAGATTCTACACCGCCAGATCGGAGCG 412
QY 121 AspIleAlaLeuLeuGlnLeuGlnGlnProValAspIleSerSerArgValHisThrVal 140
DB 413 GACATGCGCTGTGGAGCTGGAGGAGCGGTAAAGCTCTCCAGCCAGCTCCACAGCGT 472
QY 141 MetLeuProProAlaSerGlnTrpPheProProGlnMetProCysTrpValThrGlyTrp 160
DB 473 ACCCTGCGCGCTGCTCAGAGACCTTCCCGCGGAGTGGCTGCTGGGTCACTGCGTGG 532
QY 161 GlyAspValAspAspAspGlnProLeuProProPheProLeuLysGlnValLysVal 180
DB 533 GCGAGTGTGGACATGATGAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGTTC 592
QY 181 ProIleMetGlnAsnHisIleCysAspAlaLysTyrHisLeuGlnValAlaTyrThrGlyAsp 200
DB 593 CCATATATGAAAAACACCATTTGTGAGCGCAAAATACCACTTGGCGCTTACACAGGAGAC 652
QY 201 AspValArgIleIleLeuAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
DB 653 GAGTCCGCGATCTGTCGTGACGACATGCTGTGCGCGGAAACACCGGAGGAGCTATGC 712
QY 221 LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGly 240
DB 713 CAGGGGAGACTCCGAGAGGCGCGCTGTGTGCAAGGTGAATGAGCACTGGCTGCGAGGGAGC 772
QY 241 ValValSerTrpAspGlnGlyCysAlaGlnProAspArgProGlyLysIleTyrThrArgVal 260
DB 773 GTGTGAGCTGGGGCGAGGGCTGTGCGCAACCCAGCGCTGACATCTTACACCCGTGTC 832
QY 261 ThrTyrTyrLeuAspTrpIleHisIleTyrValProLysLysPro 275
DB 833 ACCTACTACTGAGCTGATCCACCACTATGTCCCAAAAAGCCG 877
RESULT 5
```

```
US-10-287-226-89
/ Sequence 89, Application US/10287226
/ Publication No. US20040086875A1
/ GENERAL INFORMATION:
/ APPLICANT: Agee, Michele L.,
/ APPLICANT: Alsbrook, John P.,
/ APPLICANT: Berghs, Constance,
/ APPLICANT: Boldog, Ferenc,
/ APPLICANT: Burgess, Catherine E.,
/ APPLICANT: Chant, John S.,
/ APPLICANT: Chaudhuri, Amitabha,
/ APPLICANT: DiPippo, Vincent A.,
/ APPLICANT: Edinger, Shlomit R.,
/ APPLICANT: Eissen, Andrew,
/ APPLICANT: Ellerman, Karen,
/ APPLICANT: Gangolli, Bsha A.,
/ APPLICANT: Gorman, Linda,
/ APPLICANT: Gerlach, Valerie,
/ APPLICANT: Ji, Weizhen,
/ APPLICANT: Kekuda, Ramesh,
/ APPLICANT: Khramtsov, Nikolai,
/ APPLICANT: Li, Li,
/ APPLICANT: Malysankar, Uriel M.,
/ APPLICANT: MacDougall, John R.,
/ APPLICANT: Mezes, Peter S.,
/ APPLICANT: Miller, Charles E.,
/ APPLICANT: Millet, Isabelle,
/ APPLICANT: Ooi, Chean Eng,
/ APPLICANT: Ort, Tatiana,
/ APPLICANT: Padigaru, Muralidhara,
/ APPLICANT: Paturejan, Meera,
/ APPLICANT: Rastelli, Luca,
/ APPLICANT: Rieger, Daniel K.,
/ APPLICANT: Rothenberg, Mark E.,
/ APPLICANT: Shenoy, Suresh G.,
/ APPLICANT: Spaderna, Steven K.,
/ APPLICANT: Spytek, Kimberley A.,
/ APPLICANT: Taupier, Jr., Raymond J.,
/ APPLICANT: Vernet, Corine A.M.,
/ APPLICANT: Zehnusen, Bryan D.,
/ APPLICANT: Zhong, Mei
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-480C
/ CURRENT APPLICATION NUMBER: US/10/287,226
/ PRIOR FILING DATE: 2002-11-04
/ PRIOR APPLICATION NUMBER: 60/334,421
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,392
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/360,148
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: 60/364,000
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/404,821
/ PRIOR FILING DATE: 2002-08-20
/ PRIOR APPLICATION NUMBER: 60/334,526
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,409
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/364,227
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/334,027
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/331,641
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 673
/ SOFTWARE: CuroSeqIst version 0.1
/ SEQ ID NO 89
/ LENGTH: 828
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
```


QY 241 ValValSerTPaSPglUGlyVCySaIaGInProaSaARgProGlyIleTyThrArVal 260
Db 773 GGGGCGACCTGGGCGGAGGCGCTGTGCGCCAGCCAGCGGCGCTGATCAACCCGCTGC 832
QY 261 ThrTyTyLeuAspTrpIleHisIstYrValProLysLysPro 275
Db 833 ACCTACTTGTGACTGGATCCACCACTATGTCTCCCAAAAAGCG 877

RESULT 8

US-10-352-684A-47
; Sequence 47, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MP102-019P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(833)
; US-10-352-684A-47

Alignment Scores:

Pred. No.: 3,79e-158 Length: 1143
Score: 1405.00 Matches: 253
Percent Similarity: 94.91% Conservative: 8
Best Local Similarity: 92.00% Mismatches: 14
Query Match: 92.92% Indels: 0
DB: 17 Gaps: 0

US-09-598-982C-52 (1-275) x US-10-352-684A-47 (1-1143)

QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArGAlaTyrrAlaAlaPro 20
Db 6 ATGCGTAATCTGTGCTGGCGGCGCTGCTGCTGCGAGCGCGCCCTACCGGCGGCGCT 65
QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlyGlnGlnAlaProArGSer 40

Db 66 GCGCCAGCGCCAGCGCCCTGCGAGCGAGTGCGATCTTGGGGGTTCAGAGAGCGCCCGAGAGC 125
QY 41 LysTrpProTrpGlnValSerLeuArgValArgAspArgTyrrTrpMetHisPheCysGly 60
Db 126 AAGTGGCCCTGGCAGGTGAGCTGAGAGTCCAGCGCCCATCTAGTAATGACATCTTCTGGCG 185
QY 61 GlySerLeuIleHisPProGlnTrpValLeuThrAlaHisCysLeuGlyProAspVal 80
Db 186 GAGTCCCTCATCCACCCCGAGGTGTGTGACCCAGAGGACCTGCTGGAGCCGAGCTC 245
QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrrTyrrGlnAspGln 100
Db 246 AAGATCTGGCGCGCCCTCAGGTGCACTGGGGAGAGACCTCTACTACAGAGACAG 305
QY 101 LeuLeuProValSerArgIleIleValHisPProGlnPheTyrrIleGlnThrGlyVal 120
Db 306 CTGCTGCCGCTCACAGGATCATGCTGTCACCCACAGTCTACACCGCCAGATCGGAGCG 365
QY 121 AspIleAlaLeuLeuGlnLeuGlnGlnProValAsnIleSerArGValHisThrVal 140
Db 366 GACATCGCCCTGTGAGCTGAGAGCGAGCGGTGAAGCTTCAGGCACGTCCACAGGCTC 425
QY 141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThrGlyTrp 160
Db 426 ACCCTGCCCCCTGCTCAGAGACCTTCCCGGGAGTCCGTGCTGCTCAGTGGCTG 485
QY 161 GlyAspValAspAsnAspGlnProLeuProProPheProLeuLysGlnValLysVal 180
Db 486 GCGCATGTGGCAATGATGAGCGCTCCACCGGCATTTCTCTGAAGCAGGTGAAGCTC 545
QY 181 ProIleMetGluAsnHisIleCysAspAlaIleTyrrHisLeuGlyAlaTyrrThrGlyAsp 200
Db 546 CCGTAATGGAACCAATTTGACCGCAATAATCACCTTGGGCTTACACGGAGAC 605
QY 201 AspValArgIleIleArgAspAspMetLeuCysAlaGlnAsnSerGlnArgAspSerCys 220
Db 606 GACGTCCGCATCGTCCGAGAGCATGCTGTGTCCGGGAGAACCCGAGGAGCATCAGC 665
QY 221 LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGly 240
Db 666 CAGGCGAGCTCCGAGAGGCGCCCTGTGTGCAAGGTGAATGACCTGCTCAGCGCGGC 725
QY 241 ValValSerTPaSPglUGlyVCySaIaGInProaSaARgProGlyIleTyThrArVal 260
Db 726 GTGTGACCTGGGAGGAGGCTGTGCCAGCCCAACCGGCTGGGATCTACACCGGTCTC 785
QY 261 ThrTyTyLeuAspTrpIleHisIstYrValProLysLysPro 275
Db 786 ACCTACTTGTGACTGGATCCACCACTATGTCTCCCAAAAAGCG 830

RESULT 9

US-10-287-226-93
; Sequence 93, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eissen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esna A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khramtsov, Nikolai,

```

APPLICANT: Li, Li'
APPLICANT: Malynkar, Uriel M.'
APPLICANT: Macdougall, John R.'
APPLICANT: Mezes, Peter S.'
APPLICANT: Miller, Charles E.'
APPLICANT: Millet, Isabelle'
APPLICANT: Ooi, Chean Eng,
APPLICANT: Ort, Tatiana.
APPLICANT: Padigaru, Muralidhara.
APPLICANT: Paturajan, Meera,
APPLICANT: Rastelli, Luca,
APPLICANT: Rieger, Daniel K.,
APPLICANT: Rothenberg, Mark E.,
APPLICANT: Shenoy, Suresh G.,
APPLICANT: Spaderna, Steven K.,
APPLICANT: Spytek, Kimberley A.,
APPLICANT: Taupier, Jr., Raymond J.,
APPLICANT: Vermet, Corine A.M.,
APPLICANT: zerhusen, Bryan D.,
APPLICANT: Zhong, Wei'
TITLE OR INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: 60/334,421
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/354,392
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/360,148
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/404,821
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 60/334,526
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/354,409
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/364,227
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/331,641
PRIOR FILING DATE: 2001-11-20
Remaining prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 673
SOFTWARE: Curoseqlist version 0.1
SEQ ID NO 93
LENGTH: 1145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (8)..(832)
US-10-287-226-93
Alignment Scores:
Pred. No.: 3,8e-158 Length: 1145
Score: 1405.00 Matches: 253
Percent Similarity: 94.91% Conservative: 8
Best Local Similarity: 92.00% Mismatches: 14
Query Match: 92.92% Indels: 0
DB: 18 Gaps: 0
US-09-598-982C-52 (1-275) x US-10-287-226-93 (1-1145)
Oy 1 MelieuSerleuLeuLeuLeuAlaLeuProValIleuAlaSerGAlaTyAlaAlaPro 20
Db 8 ATGCTGATCTGCTGCTGCTGGCGCTCCGCTCGGCGAAGCGCGCTACGCGCCCT 67
Oy 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlyGlnGlnAlaProArgSer 40
Db 68 GCCCCAGGCCAGCCCTCGAGCGAGCTGCGGCGATCGTGGGAGGTCAGAGGCCCCCGAGGAGC 127

```

QY	128	QY	61	QY	121	QY	141	QY	161	QY	181	QY	201	QY	221	QY	241	QY	261	QY	278	QY	291	QY	308	QY	321	QY	341	QY	361	QY	381	QY	401	QY	421	QY	441	QY	461	QY	481	QY	501	QY	521	QY	541	QY	561	QY	581	QY	601	QY	621	QY	641	QY	661	QY	681	QY	701	QY	721	QY	741	QY	761	QY	781	QY	801	QY	821	QY	841	QY	861	QY	881	QY	901	QY	921	QY	941	QY	961	QY	981	QY	1001	QY	1021	QY	1041	QY	1061	QY	1081	QY	1101	QY	1121	QY	1141	QY	1161	QY	1181	QY	1201	QY	1221	QY	1241	QY	1261	QY	1281	QY	1301	QY	1321	QY	1341	QY	1361	QY	1381	QY	1401	QY	1421	QY	1441	QY	1461	QY	1481	QY	1501	QY	1521	QY	1541	QY	1561	QY	1581	QY	1601	QY	1621	QY	1641	QY	1661	QY	1681	QY	1701	QY	1721	QY	1741	QY	1761	QY	1781	QY	1801	QY	1821	QY	1841	QY	1861	QY	1881	QY	1901	QY	1921	QY	1941	QY	1961	QY	1981	QY	2001	QY	2021	QY	2041	QY	2061	QY	2081	QY	2101	QY	2121	QY	2141	QY	2161	QY	2181	QY	2201	QY	2221	QY	2241	QY	2261	QY	2281	QY	2301	QY	2321	QY	2341	QY	2361	QY	2381	QY	2401	QY	2421	QY	2441	QY	2461	QY	2481	QY	2501	QY	2521	QY	2541	QY	2561	QY	2581	QY	2601	QY	2621	QY	2641	QY	2661	QY	2681	QY	2701	QY	2721	QY	2741	QY	2761	QY	2781	QY	2801	QY	2821	QY	2841	QY	2861	QY	2881	QY	2901	QY	2921	QY	2941	QY	2961	QY	2981	QY	3001	QY	3021	QY	3041	QY	3061	QY	3081	QY	3101	QY	3121	QY	3141	QY	3161	QY	3181	QY	3201	QY	3221	QY	3241	QY	3261	QY	3281	QY	3301	QY	3321	QY	3341	QY	3361	QY	3381	QY	3401	QY	3421	QY	3441	QY	3461	QY	3481	QY	3501	QY	3521	QY	3541	QY	3561	QY	3581	QY	3601	QY	3621	QY	3641	QY	3661	QY	3681	QY	3701	QY	3721	QY	3741	QY	3761	QY	3781	QY	3801	QY	3821	QY	3841	QY	3861	QY	3881	QY	3901	QY	3921	QY	3941	QY	3961	QY	3981	QY	4001	QY	4021	QY	4041	QY	4061	QY	4081	QY	4101	QY	4121	QY	4141	QY	4161	QY	4181	QY	4201	QY	4221	QY	4241	QY	4261	QY	4281	QY	4301	QY	4321	QY	4341	QY	4361	QY	4381	QY	4401	QY	4421	QY	4441	QY	4461	QY	4481	QY	4501	QY	4521	QY	4541	QY	4561	QY	4581	QY	4601	QY	4621	QY	
----	-----	----	----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	-----	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	--

Db	1031	ACCCTGGCCCCCTGGCTCAGAGACTTCCCCCGGGAGACGCTGTGGGTCATCGCTGG	1090
Qy	161	GLYASPVAlaAPaanaAPPGLuProLeuProProPheProLeuLysGlnValLysVal	180
Db	1091	GGCGATGTGGCAATGATGAGCGCTCCACCGGCATTTCTCTGAACATGTAAAGTTC	1150
Qy	181	ProIleMetGluAenHisIleCysAspAlaLysTyrHisLeuGlnValAlyrThrGlyAsp	200
Db	1151	CCCATATGGAAAAACCATTTTGTGACGCAAAATNCCACTTTGGCGCTTAACGGGAGAC	1210
Qy	201	AspValAlrGleIleIeaArgAspAspMetLeuCysAlaGlyAenSerGlnArgAspSerCys	220
Db	1211	GACGCGCGCATCGTCCGTAAGACATGCTGTGTGCGGGAAACACCGGAGGACTCANGC	1270
Qy	221	LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGly	240
Db	1271	CAGGGCGACTCCGAGGGCCCCGTGTGTGCAAGATGCACTGGCTCAGCGGGGC	1330
Qy	241	ValValSerTrpAspGluGlyCysAlaGlnProAsnArgProGlyIleIleThrArgVal	260
Db	1331	GTGGTCAGATGGGAGAGGGCTGTGCCAGGCCAACCGGCTGGCATTTACACCGGTTC	1390
Qy	261	ThrTyrTyrLeuAspTrpIleHisIleTyrValProLysLysPro	275
Db	1391	ACCTACTACTTGGACTGGATCCACCATCATGTATCCCAAAAAAGCCG	1435

RESULT 12
US-09-954-456-2126
Sequence 2126, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer

```

CURRENT APPLICATION NUMBER: US/09/954,456
?
?
CURRENT FILING DATE: 2001-09-18
?
?
PRIORITY APPLICATION NUMBER: US/60/233,617
?
?
PRIORITY FILING DATE: 2000-09-18
?
?
PRIORITY APPLICATION NUMBER: US/60/234,052
?
?
PRIORITY FILING DATE: 2000-09-20
?
?
PRIORITY APPLICATION NUMBER: US/60/234,923
?
?
PRIORITY FILING DATE: 2000-09-25
?
?
PRIORITY APPLICATION NUMBER: US/60/235,134
?
?
PRIORITY FILING DATE: 2000-09-25
?
?
PRIORITY APPLICATION NUMBER: US/60/235,637
?
?
PRIORITY FILING DATE: 2000-09-26
?
?
PRIORITY APPLICATION NUMBER: US/60/235,638
?
?
PRIORITY FILING DATE: 2000-09-26
?
?
PRIORITY APPLICATION NUMBER: US/60/235,711
?
?
PRIORITY FILING DATE: 2000-09-27
?
?
PRIORITY APPLICATION NUMBER: US/60/235,720
?
?
PRIORITY FILING DATE: 2000-09-27
?
?
PRIORITY APPLICATION NUMBER: US/60/235,840
?
?
PRIORITY FILING DATE: 2000-09-27
?
?
PRIORITY APPLICATION NUMBER: US/60/235,863
?
?
PRIORITY FILING DATE: 2000-09-27
?
?
NUMBER OF SEQ ID NOS: 2276
?
?
SOFTWARE: PatentIn version 3.0
?
?
SEQ ID NO 2126
?
?
LENGTH: 1081
?
?
TYPE: DNA
?
?
ORGANISM: Homo sapiens
?
?
US-09-954-456-2126

```

[illegible]

US-09-598-982C-52 (1-275) x US-09-954-456-2126 (1-1081)

OY	1	LeuProValIleuAlaSerArgLalArYrAlaAlaProAlaProAlaGlnAlaLeuGlnI	28
Db	2	CTGCGCGTCTGTGGCGAGCGCGGCTTACGGCGGCTTGCCTCCAGGCGAGGCGCTTCAGCGA	61
OY	29	AlaGlyTlLeValGlyGlnGlnAlaProArgSerTyrSTPProTArgIValSerLeu	48
Db	62	GTCGGGATCGTGGGGGTGAGAGAGCGCCCGAGAGCAAGTGGCCCTGGCAAGTGAAGCTTG	122
OY	49	ArgValArgAspArgTyrTTPMetHisPheCysGlyIysSerLeuIleHisProGluTyr	68
Db	122	AGAGTCGGGACCGAATCTGAATGACCTTCGGGGGGGCTCCCTCATCACCCTCCAGTGG	181
OY	69	ValIleuThrAlaAlaHisCysLeuGlyProAspValIlyAspLeuAlaThrLeuArgVal	88
Db	182	GTGCTGACCGGACGCGACACTCGGTGGGAGCGGACGTCAGATCTGGCGCGCTCAGGGGTG	244
OY	89	GlnIleuArgGlnGlnIleHisLeuTyrTyrGlnIleAspGlnLeuLeuProValSerArgTlle	106
Db	242	CAACTGGGGAGGACGACCTCTACTACCGAGCCAGCTGCTGGCGGTGACGAGGATCATC	301
OY	109	ValHisProGlnPheTyrTlleGlnThrGlyAlaAspIleAlaLeuLeuGlnLeuGlu	122
Db	302	GTGACCCACAGTTCTTACACCGGCCGATCGAGGGGACATGCGCTGTGAAGCTGGAG	363
OY	129	GluProValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThr	148
Db	362	GAGCGGGTAGAGGTCTCCAGCCACGTCACACGTCACCTGCGCCCTCGCTCAGAGACC	421
OY	149	PheProProGluIleMetProCysTyrTyrValIleThrGlyTyrGlyAspValAspAsnAspGluPro	166
Db	422	TTCCTCCCGGGGATGCGGTGTGGGTACTGGCTGTGGGCGCATGTGGACAAGAGTAGACGC	481
OY	169	IleuProProPhePheProIleuLeuGlnValIlySerValProIleMetGluAsnHisIleCys	188
Db	482	CTCCACCGCATTTCTCTGTGAAGCAGGTGAAGTCCCATTAATGGAAACACATTTGT	541
OY	189	AspAlaIlySTrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAsp	206
Db	542	GACGCAAAATACCACTTGGCGCTTACACCGGAGACGACGTCGCCATGTCTCGTAGACAC	601
OY	209	MetLeuCysAlaGlyAsnSerGlnArgAspSerCysIlyGlyAspSerGlyGlyProLeu	228
Db	602	ATCTGTGTGTCGGGGAACCCGAGAGGACTATCTACAGGCGACCTCGGAGGGGCCCTTG	661
OY	229	ValCysIlyeValAsnGlyThrTyrPheGlnAlaGlyValValSerTyrAspGlnGlyCys	248
Db	662	GTCGTGCAAGTGAATGGACCTGGCTGACAGCGGGCGGTGTCAGTGTGGCGGAGGGGCTGT	721
OY	249	AlaGlnProAsnArgProGlyTlleTyrThrArgValIleTyrTyrLeuAspTyrIleHis	266
Db	722	GCCACACCCCAACCGGCTGGCATTTACACCGCTGTCACTACTACTTGGACTGGATCCAC	781
OY	269	HisTyrValProIlyIysPro 275	
Db	782	CACATATGTCCCAAAAGCGG 802	

```

RESULT 13
US-09-960-706-680
; Sequence 680. Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; TITLE OF INVENTION: Gene Expression Profiles
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
;

```

```

; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 680
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 M33493
US-09-960-706-680

Alignment Scores:
Pred. No.: 7.36e-157 Length: 1081
Score: 1394.00 Matches: 249
Percent Similarity: 95.88% Conservative: 7
Best Local Similarity: 93.26% Mismatches: 11
Query Match: 92.20% Indels: 0
Gaps: 0

US-09-598-982C-52 (1-275) x US-09-960-706-680 (1-1081)

QY 9 LeuProValLeuAlaSerArgAlaTyrAlaAlaProAlaProValGlnAlaLeuGln 28
DB 2 CTGCCCGCTCTGGCCGAGCGCGCCCTTACGCGGCCCTTGCAGCCCTGAGCGA 61
QY 29 AlaGlyIleValGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeu 48
DB 62 GTGGGCAATGTTGGGGGTGAGAGGCCCCAGAGAGAGTGCCCTGGAGGTGAGCCTG 121
QY 49 ArgValAlaArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrp 68
DB 122 AGAGTCCCGAGCCGATCTGATGATGACATTTCTGGGGGGCTCCCTCATCACCCCAAGTGG 181
QY 69 ValLeuThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgVal 88
DB 182 GTGCTGACCGGACCGCCACTGCTGGGACCGGACGTCAAGATCTGCGCCCTCAGGGGTG 241
QY 89 GlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIle 108
DB 242 CAACTCGGGAGACGACTCTTACTACAGACAGCTGCTGCGGATCGACAGATCTC 301
QY 109 ValHisProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnLeuGln 128
DB 302 GTGCACCCACAGTTCTTACACCGCCAGATCGAGGAGCATGCCCTGCTGAGTGGAG 361
QY 129 GluProValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThr 148
DB 362 GAGCGGTGAAGGTCTCCACGCGCACACGAGTCACTGCCCCCTGCCACAGAC 421
QY 149 PheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspGluPro 168
DB 422 TTCCCCCGGGGATGCGGTGCTGAGTCACTGGGCTGGGAGATGACATGATAGGCGC 481
QY 169 LeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCys 188
DB 482 CTCCACACCGCATTTCTCTGAAAGCAGGAGGATGCCCATTAATGAAACACCACTTTGT 541
QY 189 AspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAsp 208
DB 542 GACGGAATAATACACCTTGCGCTTACACGGAAGACGAGTCCGATGCTCGTACAGAC 601
QY 209 MetLeuCysAlaGlyAsnSerGlnArgAspSerCysLysGlyAspSerGlyGlyProLeu 228
DB 602 ATGCTGTGTGCGGGAAACCGCGAGGAGCTATACCGAGGAGATCCGAGAGGCGCTTG 661
QY 229 ValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValAlaSerTrpAspGluLysCys 248
DB 662 GTGTCAAGGTGAATAGGACCTGGCTGACGCGGGGCTGCTGAGTGGGCGAGGCGTGT 721
QY 249 AlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHis 268
DB 722 GCCCAGCCCAACCGCGCTGGATCTACACCCGCTGTCACTACTTGAATGATCCAC 781
QY 269 HisTyrValProLysLeuPro 275
```

```

DB 782 CACTATGTCCCAAAAAGCCG 802

RESULT 14
US-09-873-319-427
; Sequence 427, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William R.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying drugs for and diagnosis of Benign Prostatic
; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; EARLIER FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 427
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 M33493
US-09-873-319-427

Alignment Scores:
Pred. No.: 7.36e-157 Length: 1081
Score: 1394.00 Matches: 249
Percent Similarity: 95.88% Conservative: 7
Best Local Similarity: 93.26% Mismatches: 11
Query Match: 92.20% Indels: 0
Gaps: 0

US-09-598-982C-52 (1-275) x US-09-873-319-427 (1-1081)

QY 9 LeuProValLeuAlaSerArgAlaTyrAlaAlaProAlaProValGlnAlaLeuGln 28
DB 2 CTGCCCGCTCTGGGGAGCGCGCCCTTACGCGGCCCTTGCAGCCCTGAGCGA 61
QY 29 AlaGlyIleValGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeu 48
DB 62 GTGGGCAATGTTGGGGGTGAGAGGCCCCAGAGAGAGTGCCCTGGAGGTGAGCCTG 121
QY 49 ArgValAlaArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrp 68
DB 122 AGAGTCCCGAGCCGATCTGATGATGACATTTCTGGGGGGCTCCCTCATCACCCCAAGTGG 181
QY 69 ValLeuThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgVal 88
DB 182 GTGCTGACCGGAGGACGACTGCTGGGAGCCGAGACTCAAGATCTGCGCCCTCAGGGGTG 241
QY 89 GlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIle 108
DB 242 CAACTCGGGAGACGACTCTTACTACAGACAGCTGCTGCGGATCGACAGATCTC 301
QY 109 ValHisProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnLeuGln 128
DB 302 GTGCACCCACAGTTCTTACACCGCCAGATCGAGGAGCATGCCCTGCTGAGTGGAG 361
QY 129 GluProValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThr 148
DB 362 GAGCGGTGAAGGTCTCCACGCGCACGTCACACGCTGACCTGCCCTGCTGAGAGAC 421
QY 149 PheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspGluPro 168
DB 422 TTCCCCCGGGGATGCGGTGCTGAGTCACTGGGCTGGGAGATGAGCAATGAGAGCGC 481
QY 169 LeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCys 188
```



```
Db 482 CTCGCCACCCCAATTCCTCTGAAAGCAGTGAAAGTCCCATATGAAAAACCAATTGT 541
Qy 189 AspAlaIeTYRHisLeuGIyValaTYRThrGIyAspAspValArgIleIleArgAspAsp 208
Db 542 GAGCGAATAATACCACTTGTGGCGCTTACACGGAGACGATCGCATTCGTCCGTGACGAC 601
Qy 209 MetLeuCYsaIaGIyAsnSerGIyArgAspSerCYsIySgIyAspSerGIyGIyProLeu 228
Db 602 ATGCTGTGTGCGGGAGAACCCGGAGGAGACTCATGCGAGCGAGCTCCGAGGGCCCTG 661
Qy 229 ValCYsIyValaIaSnGIyThrTrIleuGIyValaGIyValaIaSerTrpAspGIyGIyCys 248
Db 662 GTGTGCAAGGTGAATGTGACCTGTGCTGACGGCGGTGTGCTGAGGGCGAGGCTGT 721
Qy 249 AlaGIyProAsnArgProGIyIleTYRThrArgValaTYRTrpIleuAspTrpIleHis 268
Db 722 GCCCAGCCCAACCGGCTGTGACCTTACACCCGTGTCACTTACTTGGACGTGATCCAC 781
Qy 269 HisTYRValaProIySlyAspPro 275
Db 782 CACTATGTCCCAAAAAAGCCG 802
```

RESULT 15

```
US-09-873-367C-155
/ Sequence 155, Application US/09873367C
/ Publication No. US20030165839A1
/ GENERAL INFORMATION:
/ APPLICANT: Young, Paul
/ APPLICANT: Soppet, Daniel
/ APPLICANT: Endress, Gregory
/ APPLICANT: Augustus, Meena
/ APPLICANT: Ebner, Reinhard
/ APPLICANT: Carter, Kenneth
/ TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
/ FILE REFERENCE: 689290-64
/ CURRENT APPLICATION NUMBER: US/09/873,367C
/ PRIOR FILING DATE: 2003-04-29
/ PRIOR APPLICATION NUMBER: U.S. 60/236,891
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: U.S. 60/236,842
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: U.S. 60/244,867
/ PRIOR FILING DATE: 2000-11-01
/ PRIOR APPLICATION NUMBER: U.S. 60/245,084
/ PRIOR FILING DATE: 2000-11-01
/ NUMBER OF SEQ ID NOS: 1067
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 155
/ LENGTH: 1081
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-873-367C-155
```

Alignment Scores:

```
Pred. No.: 7.36e-157 Length: 1081
Score: 1394.00 Matches: 249
Percent Similarity: 95.88 Conservative: 7
Best Local Similarity: 93.26 Mismatches: 11
Query Match: 92.20 Indels: 0
DB: 10 Gaps: 0
```

US-09-598-982C-52 (1-275) x US-09-873-367C-155 (1-1081)

```
Qy 9 LeuProValLeuAlaSerArgAlaTYRAlaAlaProAlaProValaGIyAlaLeuGIyIn 28
Db 2 CTGCCCGTCTCGCGAGCCGCGCTTACGCGCCCTGCGCCAGGCCCTGTGACGCA 61
Qy 29 AlaGIyIleValaGIyGIyGIyGIyAlaProArgSerIyTrpProTrpGIyValaSerLeu 48
Db 62 GTGGGATGTGTGGGGGTGAGAGGCCCCCGAGAGCAAGTGGCCCTGTGAGGTGAGCTG 121
```

```
Qy 49 ArgValaIaArgAspArgTYRTrpMetHisPheCYsGIyIySerLeuIleHisProGIyInTrp 68
Db 122 AGAGTCCCGGACCGGATCTGATGATGATGATCTTGGCGGGGCTCCCTCATCCACCCCGAGGG 181
Qy 69 ValLeuThrAlaAlaHisCYsLeuGIyProAspValaIyAspLeuAlaThrLeuArgVal 88
Db 182 GTGTGACCGGACCGGACCTGTGGAGACGGAGCGTCAAGATCTGGCCCTCAAGGTTG 241
Qy 89 GluLeuArgGIyGIyHisLeuTYRTrpIleAspGIyIleuLeuProValaSerArgIleIle 108
Db 242 CAACGCGGGAGACACACTTCTACTACAGGACGAGCTGTGCGCGGTGACGAGATCATTC 301
Qy 109 ValHisProGIyPheTYRTrpIleIleGIyThrGIyAlaAspIleAlaLeuLeuGIyLeuGIy 128
Db 302 GTGCAACCCACAGTTCTTACACCGCCAGATCGAGGAGCATCGCTGTGAGAGCTGAG 361
Qy 129 GluProValaSnIleSerSerArgValaHisThrValaMetLeuProProAlaSerGIyInThr 148
Db 362 GAGCGGTGAAGGTCTTCCAGCCAGCTTCCACAGGTACACCTTGTCCCTGTGCTGAGAGAC 421
Qy 149 PheProProGIyMetProCYsTrpValaThrGIyTrpGIyAspValaAspAsnAspGIyPro 168
Db 422 TTCCCGCGGGGATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
Qy 169 LeuProProProPheProLeuIySgIyValaIyValaIyValaIyValaIyValaIyVala 188
Db 482 CTCGCCACCCCAATTCCTCTGAAAGCAGTGAAAGTCCCATATGAAAAACCAATTGT 541
Qy 189 AspAlaIeTYRHisLeuGIyValaTYRThrGIyAspAspValArgIleIleArgAspAsp 208
Db 542 GAGCGAATAATACCACTTGTGGCGCTTACACGGAGACGATCGCATTCGTCCGTGACGAC 601
Qy 209 MetLeuCYsaIaGIyAsnSerGIyArgAspSerCYsIySgIyAspSerGIyGIyProLeu 228
Db 602 ATGCTGTGTGCGGGAGAACCCGGAGGAGACTCATGCGAGGAGACTCCGAGGGCCCTG 661
Qy 229 ValCYsIyValaIaSnGIyThrTrIleuGIyValaGIyValaIaSerTrpAspGIyGIyCys 248
Db 662 GTGTGCAAGGTGAATGTGACCTGTGCTGACGGCGGTGTGCTGAGGGCGAGGCTGT 721
Qy 249 AlaGIyProAsnArgProGIyIleTYRThrArgValaTYRTrpIleuAspTrpIleHis 268
Db 722 GCCCAGCCCAACCGGCTGTGACCTTACACCCGTGTCACTTACTTGGACGTGATCCAC 781
Qy 269 HisTYRValaProIySlyAspPro 275
Db 782 CACTATGTCCCAAAAAAGCCG 802
```

Search completed: August 28, 2005, 01:30:05
Job time : 622 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 27, 2005, 23:30:16 ; Search time 166 Seconds
(without alignments)
2419.226 Million cell updates/sec

Title: US-09-598-982C-52
Perfect score: 1512
Sequence: 1 MSLULLALPTLASRAVAAP.....ITRTVYVLDWIIHYVRKP 275

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL=frame+g2n.model -DEV=xlp
-O=/cgn2_1/USPRO/spool_p/US09598982/rnat_25082005_165826_1568/app_query.fasta_1.455
-DB=Issued_Patents_NA -QFMT=fastcap -SUFFIX=xrml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982@cgn_1_1_105@rnat_25082005_165826_1568 -NCPD=6 -ICPD=3
-NO MMAP -LARGEREQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1512	100.0	1154	2	US-09-016-366A-16
2	1512	100.0	1154	2	US-08-978-404B-11
3	1402	92.7	1137	2	US-09-016-366A-18
4	1402	92.7	1137	2	US-08-978-404B-13
5	1400	92.6	1128	2	US-09-016-366A-20
6	1400	92.6	1128	2	US-08-978-404B-15
7	1394	92.2	1081	2	US-09-016-366A-22
8	1394	92.2	1081	2	US-08-978-404B-17
9	1394	92.2	1081	4	US-09-917-254-50
10	1284	84.9	771	3	US-09-079-970A-1
11	1284	84.9	771	3	US-09-079-970A-4
12	1134	75.0	1031	2	US-08-978-404B-1

13	1133	74.9	1108	2	US-09-016-366A-14	Sequence 14, Appl
14	1133	74.9	1108	2	US-08-978-404B-20	Sequence 20, Appl
15	1118.5	74.0	2259	2	US-08-845-998-3	Sequence 3, Appl
16	1118.5	74.0	2259	3	US-09-206-537-3	Sequence 3, Appl
17	1118.5	74.0	2259	3	US-09-430-854-3	Sequence 7, Appl
18	1109.5	73.4	1219	3	US-08-978-404B-7	Sequence 24, Appl
19	1105	73.1	1097	2	US-08-978-404B-4	Sequence 4, Appl
20	1105	73.1	1103	2	US-09-016-366A-24	Sequence 5, Appl
21	1080.5	71.5	2218	2	US-08-845-998-5	Sequence 5, Appl
22	1080.5	71.5	2218	3	US-09-430-854-5	Sequence 5, Appl
23	1080.5	71.5	2218	3	US-09-016-366A-13	Sequence 19, Appl
24	986	65.2	3757	2	US-08-978-404B-19	Sequence 9, Appl
25	986	65.2	3757	2	US-08-978-404B-9	Sequence 1, Appl
26	892.5	59.0	2397	2	US-08-978-404B-1	Sequence 1, Appl
27	886.5	45.4	1095	2	US-08-978-404B-8	Sequence 1, Appl
28	886.5	45.4	1110	3	US-08-978-404B-1	Sequence 1, Appl
29	570.5	37.7	1212	4	US-09-620-312D-431	Sequence 43, App
30	560.5	37.1	980	4	US-09-023-942A-30	Sequence 30, Appl
31	555	36.7	1130	3	US-09-386-653A-8	Sequence 8, Appl
32	553.5	36.6	933	4	US-09-023-942A-29	Sequence 29, Appl
33	553.5	36.6	1613	4	US-09-387-375-1	Sequence 1, Appl
34	553.5	36.6	1613	4	US-10-041-400A-1	Sequence 1, Appl
35	553.5	36.6	1613	4	US-10-042-091A-1	Sequence 1, Appl
36	535	35.4	1130	4	US-09-387-375-8	Sequence 8, Appl
37	535	35.4	1130	4	US-10-041-400A-8	Sequence 8, Appl
38	535	35.4	1130	4	US-10-042-091A-8	Sequence 8, Appl
39	530.5	35.1	1378	4	US-09-907-794A-262	Sequence 262, App
40	530.5	35.1	1378	4	US-09-905-125A-262	Sequence 262, App
41	530.5	35.1	1378	4	US-09-902-775A-262	Sequence 262, App
42	530.5	35.1	1378	4	US-09-906-700-262	Sequence 262, App
43	530.5	35.1	1378	4	US-09-903-603A-262	Sequence 262, App
44	530.5	35.1	1378	4	US-09-904-920A-262	Sequence 262, App
45	530.5	35.1	1378	4	US-09-909-064-262	Sequence 262, App

ALIGNMENTS

RESULT 1
US-09-016-366A-16
; Sequence 16, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESS: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037.090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441

```
TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-016-366A-16

Alignment Scores:
Pred. No.: 1,56e-156 Length: 1154
Score: 1512.00 Matches: 275
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-598-982C-52 (1-275) x US-09-016-366A-16 (1-1154)
QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaAlaPro 20
DB 18 ATCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 77
QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyTleValGlyGlnGlnAlaProArgSer 40
DB 78 GCCCAGTCAGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 137
QY 41 LysTyrProTyrGlnValSerLeuArgValArgAspArgTyrTyrMetHisPheCysGly 60
DB 138 AAGTGGCCCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 197
QY 61 GlySerLeuLeuHisProGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
DB 198 GGTCTCCCTCATCACCACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 257
QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGln 100
DB 258 AAGGATCTGGCCACCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 317
QY 101 LeuLeuProValSerArgTleValHisProGlnPheTyrTleGlnThrGlyAla 120
DB 318 CTGCTGCAGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 377
QY 121 Asp1AlaLeuLeuGlnLeuGlnGlnProValAsn1LysSerArgValHisThrVal 140
DB 378 GATATCGCCCTGCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
QY 141 MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTyrVal1ThrGlyTyr 160
DB 438 ATCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 497
QY 161 GlyAspValAspAsnAspGlnProLeuProProProPheProLeuGlnValLysVal 180
DB 498 GCGGATGTGACATATGAGCCCTCCACCGCCATTTCCCTGAAGACGAGGAGGAGGAGGAG 557
QY 181 Pro1LemecGluAsnHis1LysCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
DB 558 CCATATATGAAAAACCACTTTGTGACGCAAAATATACACTTGGCCGCTTACAGGAGAGAC 617
QY 201 AspValArgTle1LysArgAspAspMetLeuCysAlGlyAsnSerGlnArgAspSerCys 220
DB 618 GAGGTCGCGATCATCGTGTGACGATGCTGTGCGGGAACAGCAGAGGAGGAGGAGGAGG 677
QY 221 LysGlyAspSerLysGlyProLeuValCysLysValAsnGlyTyrTyrLeuGlnAlaGly 240
DB 678 AAGGGGCACTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 737
QY 241 ValValSerTyrAspGlnGlyCysAlaGlnProAsnArgProGlyTyrTyrThrArgVal 260
DB 738 GTGTGACGCTGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 797
QY 261 ThrTyrTyrLeuAspTyrTyrLysHisTyrValProLysLysAspPro 275
```

```
DB 798 ACTTACTGACTGAGTGCACCATATGATCCCAAAAAGCCG 842
RESULT 2
US-08-978-404B-11
; Sequence 11, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-978-404B-11

Alignment Scores:
Pred. No.: 1,56e-156 Length: 1154
Score: 1512.00 Matches: 275
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-598-982C-52 (1-275) x US-08-978-404B-11 (1-1154)
QY 1 MetLeuSerLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaAlaPro 20
DB 18 ATCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 77
QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyTleValGlyGlnGlnAlaProArgSer 40
DB 78 GCCCAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 137
QY 41 LysTyrProTyrGlnValSerLeuArgValArgAspArgTyrTyrMetHisPheCysGly 60
DB 138 AAGTGGCCCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 197
QY 61 GlySerLeuLeuHisProGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
DB 198 GGTCTCCCTCATCACCACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 257
```

QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGln 100
 DB 258 AAGATCTGGCCACCTCTGAGGTGCACTGGCGAGACGACCTTACTACAGAGACAG 317
 QY 101 LeuLeuProValSerArgTlleIleValHisProGlnPheTyrTlleIleGlnThrGlyAla 120
 DB 318 CTGCTGCAGTACAGAGATCATCTGTGACACCAAGTTCTACATCATCATGAGCTGAGACG 377
 QY 121 AspIleAlaLeuLeuGlnLeuGlnLupProValAsnIleSerSerArgValHisThrVal 140
 DB 378 GATATCGCCCTGCTGAGCTGAGAGAGCCCGTGAACATCTCCAGCCGGTCCACAGGTC 437
 QY 141 MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTyrValThrGlyTyr 160
 DB 438 ATGCTGCCCTGCTGCTGAGACCTTCCCTCCGGGAGTCCCTGCTGGGTCACTGGCTGG 497
 QY 161 GlyAspValAspAsnAspGlnLupProLeuProProProPheProLeuLysGlnValLysVal 180
 DB 498 GGCAGTGTGACAAATGATGAGCCCTCCCAACCGCATTTCCCTGAGAGAGGTGAAGGTC 557
 QY 181 ProIleMetGluAsnHisIleCysAspAlaLysTyrHisIleGlnValAlaTyrThrGlyAsp 200
 DB 558 CCAATAAATGAAACCACTTTGTGACGCAAAATACCACTTGGCGCTTACACGGGAGAC 617
 QY 201 AspValArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
 DB 618 GACGTCCCGCATCATCTGTGACACATGCTGTGTCCGGGACAGCCAGAGGATCTCTGTC 677
 QY 221 LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTyrLeuGlnAlaGly 240
 DB 678 AAGGCGACTGTGAGGGCCCTGGTGTGCAAGTGAATGTGACACTGGGTACAGCGGAGC 737
 QY 241 ValValSerTyrAspGlnGlyCysAlaGlnProAsnArgProGlyTyrLeuTyrThrArgVal 260
 DB 738 GTGGTACGTGGAGAGAGGCTGTGCTGCCAGCCCAACCGGCTGGCATCTACACCCGTGTC 797
 QY 261 ThrTyrTyrLeuAspTyrIleHisIleTyrValProLysLysPro 275
 DB 798 ACCTACTTGTGACTGATGATCCACCATATGTCTCCCAAAAAGCCG 842
 RESULT 3
 US-09-016-366A-18
 ; Sequence 18, Application US/09016366A
 ; Patent No. 5955431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7093

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1137 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-016-366A-18
 Alignment Scores:
 Pred. No.: 1,93e-144 Length: 1137
 Score: 1402.00 Matches: 252
 Percent Similarity: 95.24% Conservative: 8
 Best Local Similarity: 92.31% Mismatches: 13
 Query Match: 92.72% Indels: 0
 DB: 2 Gaps: 0
 US-09-598-982C-52 (1-275) x US-09-016-366A-18 (1-1137)
 QY 3 SerLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaAlaProAlaPro 22
 DB 3 AATCGTGTGCTGTGGGCTGCTCCGCTCGAGCGCGGCTTACGCGGCTGCCCCCA 62
 QY 23 ValGlnAlaLeuGlnGlnAlaGlyTyrLeuValGlyGlnGlnAlaProArgSerLysTyr 42
 DB 63 GGCAGCGCCCTGACGAGGTGGGATGTCGGGGGTGACAGAGGCCCCCAGAGCAATGTG 122
 QY 43 ProTyrGlnValSerLeuArgValArgAspArgTyrTyrMetHisPheCysGlyGlySer 62
 DB 123 CCTGTGAGGTGAGCTGAGGTGCTGACGCGCCCATCTGAGTGCATTTGTGGGGGCTCC 182
 QY 63 LeuIleHisProGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspValLysAsp 82
 DB 183 CTCATCCACCCCGAGTGGGTCTGACCGAGCGCAGCTGCGGAGCGGACGTCAGAGAT 242
 QY 83 LeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuLeu 102
 DB 243 CTGGCGCGCTTCAGAGGTGCACTCGGGAGAGACCTCTACTACAGACCACTGCTGTG 302
 QY 103 ProValSerArgIleIleValHisProGlnPheTyrTlleIleGlnThrGlyAlaAspIle 122
 DB 303 CCGGTGACAGATCATCTGTGACCCACAGTTCTTACACCGCCCAATCGAGCGGACATC 362
 QY 123 AlaLeuLeuGlnLeuGlnLupProValAsnIleSerSerArgValHisThrValMetLeu 142
 DB 363 GCGCTGTGAGGTGAGAGACCGGTGAGGTCTCCAGCCACGTCACACGATCACCGCTG 422
 QY 143 ProProAlaSerGlnThrPheProProGlyMetProCysTyrValThrGlyTyrGlyAsp 162
 DB 423 CCCCCTGCTCAGAGACCTTCCCTCCGCGGATGCGGTGCTGCTGCTGCTGCTGCTGCTG 482
 QY 163 ValAspAsnAspGlnLupProLeuProProPheProLeuLysGlnValLysValProIle 182
 DB 483 GTGACATGATGAGCGGCTTCCACCGCATTTCTTGAAGACGCTGAGAGGTCCCATTA 542
 QY 183 MetGluAsnHisIleCysAspAlaLysTyrHisLeuGlnAlaTyrThrGlyAspAspVal 202
 DB 543 ATGGAACCACTTTGTGACGAAATATACCACTTGGCGCTTACAGGAGAGAGAGCTC 602
 QY 203 ArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCysLysGly 222
 DB 603 CGCATGTGCTGCTGAGCATCTGTGTGCGCGGAAACCCGAGAGGACTCATGTCAGAGGC 662
 QY 223 AspSerGlyGlyProLeuValCysLysValAsnGlyThrTyrPheGlnAlaGlyValVal 242
 DB 663 GACTCCGAGAGGCGCCCTGTGTGCAAGTGAATGACACTGTGCTGACAGCGGCGGTGTC 722
 QY 243 SerTyrAspGlnGlyCysAlaGlnProAsnArgProGlyTyrTyrThrArgValThrTyr 262

DB 723 AGCTGGGCGAGGCTGTGTGCCAGCCCAACGGGCTGGCATCTACCCGTGTACCTTAC 782

QY 263 TTTTLeuAspTTP1LeuHisTyrValProLysLysPro 275

DB 783 TACTTGACTGGATCCACCATATGTCTCCCAAAAAGCCG 821

RESULT 4

US-08-978-404B-13

; Sequence 13, Application US/08978404B

; Patent No. 5968782

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES

TITLE OF INVENTION: FIBRINOGEN

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,404B

FILING DATE: 25-NOV-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032,354

FILING DATE: 04-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7090

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 1137 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-978-404B-13

Alignment Scores:

Pred. No.: 1,93e-144 Length: 1137

Score: 1402.00 Matches: 252

Percent Similarity: 95.24% Conservative: 8

Best Local Similarity: 92.31% Mismatches: 13

Query Match: 92.72% Indels: 0

DB: 2 Gaps: 0

US-09-598-982c-52 (1-275) X US-08-978-404B-13 (1-1137)

QY 3 SerLeuLeuLeuLeuLeuLeuProValLeuAlaSerArgAlaTyrAlaAlaProAlaPro 22

DB 3 AATCTGCTGCTGTGGGCTGCCCTGTCTGGCGAGCGCCCTTACCCGCGCTGCCCCA 62

QY 23 ValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlnGlnAlaProArgSerLysTyr 42

DB 63 GGCAGAGCCCTTGAGGAGCTGCGCATGTCGGGGGTCAAGAGGCCCCCAAGAGAGTGG 122

QY 43 ProTyrGlnValSerLeuArgValArgAspArgTyrTyrMetHisPheCysGlyLysSer 62

DB 123 CCTTGCGAGGTGAGCTCGAGAGTCCACGGCCCATATCGATGATGATCTTCTGGGGGCTCC 182

QY 63 LeuIleHisPheGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspValLysAsp 82

DB 183 CTGATCCACCCCACTGGGTGTCTGACCGACGCACTGCGGGAGCCGAGCTCAAGAT 242

QY 83 LeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAlaAspGlnLeuLeu 102

DB 243 CTGGCCGCTTCAGAGGTGCAACTGGGGAGCAGACACTCTTACTACAGAGACAGCTGCTG 302

QY 103 ProValSerArgIleIleValHisPheGlnPheTyrIleIleGlnThrGlyAlaAspIle 122

DB 303 CGGTCAGACAGGATCATGTGCACCACAGTTCTTACACCGCCGATGTGAGCGGACATTC 362

QY 123 AlaLeuLeuGlnLeuGlnGlnProValAsnIleSerSerArgValHisThrValMetLeu 142

DB 363 GCGCTGCTGGAGCTGGAGAGCGGCTGAGCGTCTCAGCCACGTCACACGATCACTCTG 422

QY 143 ProProAlaSerGlnThrPheProProGlyMetProCysTyrValThrGlyTyrGlyAsp 162

DB 423 CCCCCTGCTCAGAGACTTCCCCCGGGGATGCCGTCTGGTCACTGCGGGGCGAT 482

QY 163 ValAspAsnAspGlnProLeuProProProPheProLeuLysGlnValLysValProIle 182

DB 483 GTGACAAATGATGAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGTCCCACTA 542

QY 183 MetGluAsnHisIleCysAspAlaIleTyrHisLeuGlyAlaTyrThrGlyAspAspVal 202

DB 543 ATGAAAAACACATTGTGACGCAAAATVACCACTTGCGCTTACACGGAGACGACCTC 602

QY 203 ArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCysLysGly 222

DB 603 CGCATCGTCCTGACGACGATGCTGTGTCCGGGAACACCCGAGGAGATCTCATGCGAGGC 662

QY 223 AspSerGlyGlyProLeuValCysLysValAsnGlyThrTyrPleuGlnAlaGlyValAl 242

DB 663 GACTCCGAGAGGCGCCCTGCTGTGCAAGGTGAATGGCACCTGGCTGCAAGCGGCGTGTCT 722

QY 243 SerTyrAspGlnGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyr 262

DB 723 AGCTGGGCGAGGCTGTGTGCCAGGCCAACCGGCTGGCATCTTACACCGTGTCACTAC 782

QY 263 TTTTLeuAspTTP1LeuHisTyrValProLysLysPro 275

DB 783 TACTTGACTGGATCCACCATATGTCTCCCAAAAAGCCG 821

RESULT 5

US-09-016-366A-20

; Sequence 20, Application US/09016366A

; Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,366A

FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,090

FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

Db	122	TGACCCTGGCAGGGTGAAGCTCGAAGATCCACGGCCCATCTGGATATCACTTCTGGGGGGCC	181
Qy	62	SeLeuLleHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspValLys	81
Db	182	TCCTCATCCACCCCAAGTGGGTGCTGACCGAGGGCACTGGGGAGCCGAACTCAAG	241
Qy	82	AspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTrpGlnAspGlnLeu	101
Db	242	GATCTGGCCGCCCTTCAGGGGTGGCACTGGGGGAGCAGCACTCTACTACAGAACCACTG	301
Qy	102	LeuProValSerArgGlleIleValHisProGlnPheTyrIleIleGlnThrGlyAlaAsp	121
Db	302	CTCCCGGTGACGAGGATCATCTGGACCCACAGTCTTACACCGCCCAATGGAGCGGAC	361
Qy	122	IleAlaLeuLeuGlnIleuGlnGlnIleuProValaAsnIleSerArgValHisThrValMet	141
Db	362	ATGGCCCTGTGGAGCTGGAGAGACCGGTGAAGGCTCTCAAGCAGCTCAACGGTCAAC	421
Qy	142	LeuProProAlaSerGlnThrPheProProGlyMetProCysTrpValThrGlyTrpGly	161
Db	422	CTGCCCCCTGCTCAGAGCTGGAGAGACCGGTGAAGGCTCTCAAGCAGCTCAACGGTCAAC	481
Qy	162	AspValAlaAspAsnAspGlnLeuProPheProPheProLeuLysGlnValLysValPro	181
Db	482	GAGTGTGACATATATAGAGCGCTCCACCGCATTTCTCTGAAGCAGTATGAAGTCCC	541
Qy	182	IleMetGlnAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAsp	201
Db	542	ATATATGGAAGAACCATATTTGTATCGCGAATAATACCACTTTGGGGCTTACAGGAGAC	601
Qy	202	ValArgGlleIleArgAspAsnMetLeuCysAlaGlnProAsnArgProGlyIleTyrThrArgValThr	221
Db	602	GTCGGATGCTCGGTACACATGCTGTGTGCGGGAAACCCCGAGGAGACTCATGTCAG	661
Qy	222	GlyAspSerGlyValYrProLeuValCysLysValaAsnGlyThrTrpLeuGlnAlaGlyVal	241
Db	662	GCGGACTCCGGAGGGCCCTGTGTGTGCAAGTGAATGGCACTGTGTGCAAGCGGGCTG	721
Qy	242	ValSerTrpAspGlnGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThr	261
Db	722	GTCAGCTGGGGGAGAGGCTGTGTGCCAGCCACCGGCTGGGACTATACACCGGTGAC	781
Qy	262	TyrTrpLeuAspTrpIleHisThrValProLysLysPro	275
Db	782	TACTACTGTGACTGATCCACCATATGTGCCCAAAAAGCCG	823
RESULT 7			
US-09-016-366A-22			
Sequence 22, Application US/09016366A			
Patent No. 5955431			
GENERAL INFORMATION:			
APPLICANT: Stevens, Richard L.			
APPLICANT: Huang, Chifu			
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE			
TITLE OF INVENTION: INHIBITORS			
NUMBER OF SEQUENCES: 65			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.			
STREET: 600 Atlantic Avenue			
CITY: Boston			
STATE: MA			
COUNTRY: U.S.A.			
ZIP: 02210-2211			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette			
COMPUTER: IBM Compatible			
OPERATING SYSTEM: DOS			
SOFTWARE: FastSeq for Windows Version 2.0			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/016,366A			
FILING DATE: January 30, 1998			
CLASSIFICATION: 530			
PRIOR APPLICATION DATA:			

[illegible]

229 ValCysIysValAaenGlyThrTrpLeuGlnAlaGlyValIleSerTrpAspGluGlyCys 248
662 GTGTCAAGAGTAATGCGACCTGGCTGCGAGCGGCGGTAGCTGGGCGCAAGGCGCTGT 721
249 AlaGlnProAsnArgProGlyIleTyThrArgValIleTyTrpLeuAspTrpIleHis 268
722 GCCCAGCCCAACCGGCGCTGGCATCAACCGGTGTCACTACTACTGTGAGCTGATCCAC 781
269 HisTyValProIysValysPro 275
782 CACTATGTCCCCAAAAGCCG 802
RESULT 8
US-08-978-404B-17
Sequence 17, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-17
Alignment Scores:
Pred. No.: 1,35e-143 Length: 1081
Score: 1394.00 Matches: 249
Percent Similarity: 95.88
Best Local Similarity: 93.26 Mismatches: 11
Query Match: 92.20 Indels: 0
Gaps: 0
US-09-598-982C-52 (1-275) x US-08-978-404B-17 (1-1081)
QY 9 LeuProValLeuAlaSerArgAlaTrpAlaAlaProAlaProValAlaGlnAlaLeuGln 28
DB 2 CTGCCCCGTCTGGCGAGCGCGCTTAAGCGGCCCTCCAGGCCAGGCGCCCTGCGAGCA 61
QY 29 AlaGlyIleValGlyGlyGlnGlnAlaProArgSerIleTrpProTrpGlnValSerLeu 48
DB 62 GTGGGCGATCGTTGGGGGTCAAGAGGCGCCCGCAGAGCAACTGGCCCTGGCGAGCTG 121

49 ArgValArgAspArgTyTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrp 68
122 AGAGTCGCGCAGCATCTGATGACTTCTGCGGGGAGCTCCCTCATTCACCCCCAGAGG 181
69 ValLeuThrAlaAlaHisCysLeuGlyProAspValIysAspLeuAlaThrLeuArgVal 88
182 GTGCTGACCGGAGCGCACTGGGTGGAGCCGAGCTCAAGAGATCTGGCGCCCTCAGGGTG 241
89 GlnLeuArgGlnGlnHisLeuTyTrpGlnAspGlnLeuProValSerArgIleIle 108
242 CAACCTGGGGAGCAGCACTCTACTACAGGACCGAGCTGCGCGGTCTAGCAGATCATTC 301
109 ValHisProGlnPheTyTrpIleGlnThrGlyAlaAspIleAlaLeuLeuGlnLeuGln 128
302 GTGACCCACAGTTCTACACCGCCAGATCGAGCGAGCATGCGCTGTGGAGCTGGAG 361
129 GluProValAenIleSerSerArgValHisThrValMetLeuProValAspGlnThr 148
362 GAGCTCGTGAAGGTCTCCAGCCAGCTCCACAGGTCACCGTCCGCTGCTCAGAGACC 421
149 PheProProGlyMetProCysTrpValIleGlyTrpGlyAspValAspAspGluPro 168
422 TTCCCGCGGGAGATGCGGTGCTGGGTCACTGGCGGCGATGTGACATGATGAGCGC 481
169 LeuProProProPheProLeuValGlnValIysValProIleMetGluAspHisIleCys 188
482 CTCCACCGCATTTCTCTGAGCAGGTGAAGGTCCCATTAATGAAGAACACATTTGT 541
189 AspAlaIysTyTrpHisLeuGlyAlaTyThrGlyAspAspValArgIleIleArgAspAsp 208
542 GAGCGAAATACCACTTTGGGCTTACACGGGAGACAGACGTCCCATGTGTCGAGACAC 601
209 MetLeuCysAlaGlyAsnSerGlnArgAspSerCysIysGlyAspSerGlyGlyProLeu 228
602 ATGCTGTGTGCGGGAAACACCGGAGGAGCATCATGACAGGCGGAGCTCGGAGGCGCTGT 661
229 ValCysIysValAaenGlyThrTrpLeuGlnAlaGlyValIleSerTrpAspGluGlyCys 248
662 GTGTCAAGGTGAATGCACTGCTGAGCGGCGGTGTGACTGTGGGCGAGGCGCTGT 721
249 AlaGlnProAsnArgProGlyIleTyThrArgValIleTyTrpLeuAspTrpIleHis 268
722 GCCCAGCCCAACCGGCGCTGGCATCAACCGGTGTCACTACTACTGTGAGCTGATCCAC 781
269 HisTyValProIysValysPro 275
782 CACTATGTCCCCAAAAGCCG 802
RESULT 9
US-09-917-254-50
Sequence 50, Application US/09917254
Patent No. 6703204
GENERAL INFORMATION:
APPLICANT: Mutter, George
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/7224 (JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50
LENGTH: 1081
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-917-254-50
Alignment Scores:
Pred. No.: 1,35e-143 Length: 1081
Score: 1394.00 Matches: 249

Percent Similarity: 95.88%
 Best Local Similarity: 93.26%
 Query Match: 92.20%

Conservative: 7
 Mismatches: 11
 Indels: 0
 Gaps: 0

US-09-598-982C-52 (1-275) x US-09-917-254-50 (1-1081)

```

QY 9 LeuProValIleuAlaSerArgAlaYrAlaAlaProAlaProValAlaLeuGln 28
Db 2 CTGCGGCTCTGGAGAGCCGCGCTAGCGCGCCCTGCGCCAGAGCCCTGAGCGA 61
QY 29 AlaGlyTleValGlyGlnGlnAlaProArgSerTyrProProGlnValSerLeu 48
Db 62 GTGGGACCTCTGGGGGTCAAGAGGCCCGAGAGCAAGTGGCCCTGGCAGGACCTG 121
QY 49 ArgValArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrp 68
Db 122 AGAGTCCGCGCAGATGCTGAGTGCATCTTGGGGGGCTCTCATCCACCCCGAGTGG 181
QY 69 ValIleuThrAlaAlaHisCysLeuGlyProAspValIleAspLeuAlaThrIleuArgVal 88
Db 182 GTGCTGACCGCAGCGACCTGCGGAGACCGAGCTCAAGATCTGGCCGCTCAGGGTGG 241
QY 89 GlnIleuArgGlnGlnHisLeuTyrTyrGlnAspGlnIleuLeuProValSerArgIleIle 108
Db 242 CAACTGGGAGAGAGACCTCTACTACAGACAGACAGCTGCTGCGGTCAAGATCATC 301
QY 109 ValHisProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnLeuGln 128
Db 302 GTGCAACCAACAGTTCACACCGCCAGATGGAGCGGACATGCCCTGCTGGAGCTGGAG 361
QY 129 GluProValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThr 148
Db 362 GAGCCGGGTGAAGGCTCTCCAGCCAGTCCACACGAGTCACTGCGCCCTGCTCAGAGACC 421
QY 149 PheProProGlnMetProCysTrpValThrGlyTyrGlyValAspValAspAspGluPro 168
Db 422 TTCCCGCGGGAGTCCGTCTGGTCTACCTGGCTGGGGCGATGGACAATGATGAGCGC 481
QY 169 LeuProProProPheProLeuLysGlnValIleValProIleMetGlnAsnHisIleCys 188
Db 482 CTCGCCAGCGCATTTCTCTGAGAGAGTGAAGTCCCAATATGAAAAACCATTTGT 541
QY 189 AspAlaIleTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAsp 208
Db 542 GAGCAAAATACACCTTGGCGCTTACACGAGAGACGACGTCGCGCATCTGCGTGAAGAC 601
QY 209 MetLeuCysAlaGlyAsnSerGlnArgAspSerCysIleGlyAspSerGlyGlyProLeu 228
Db 602 ATGCTGTGTCGGGGAACACCGAGAGGACTCATGCGAGGCGACATCCGAGGGGCCCTG 661
QY 229 ValCysIleValAsnGlyTyrTrpLeuGlnAlaGlyValValSerTrpAspGlnGlyCys 248
Db 662 GTGTGCAAGTGAATGGACCTGGCTGCAAGCGGGCGTGTGCTGCTGGCGAGGGCTGT 721
QY 249 AlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHis 268
Db 722 GCCAGCGCAACGCGCTGGCATCTACACCGGTGTCACTACTACTGAGCTGGATCCAG 781
QY 269 HisTyrValProLysLysPro 275
Db 782 CACTATGTCCCAAAAAGCG 802

```

RESULT 10

US-09-079-970A-1

; Sequence 1, Application US/09079970A
 ; Patent No. 6274366
 ; GENERAL INFORMATION:
 ; APPLICANT: Maffitt, Mark A.
 ; APPLICANT: Niles, Andrew L.
 ; APPLICANT: Haak-Frendscho, Mary
 ; TITLE OF INVENTION: Enzymatically-Active Recombinant Human
 ; TITLE OF INVENTION: Beta-Trypsin and Method of Making Same

```

; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Intellectual Property Department
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,970A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506, 073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..735
; US-09-079-970A-1

```

Alignment Scores:

Pred. No.:	9,556-132	Length:	735
Score:	1284.00	Matches:	227
Percent Similarity:	95.10%	Conservative:	6
Best Local Similarity:	92.65%	Mismatches:	12
Query Match:	84.92%	Indels:	0
DB:	3	Gaps:	0

US-09-598-982C-52 (1-275) x US-09-079-970A-1 (1-735)

```

QY 31 ILeValGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50
Db 1 ATGTCGGGGGTCAAGAGGCCCGCCAGAGCAAGTGGCCCTGGCAAGTATGCTGAC 60
QY 51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70
Db 61 CACGGCCCATCTGATGACATCTTGGCGGGCTCTCTCATCCACCCAGTGGGTGCTG 120
QY 71 ThrAlaAlaHisCysLeuGlyProAspValIleAspLeuAlaThrLeuArgValGlnLeu 90
Db 121 ACCGCGCGCCTGGGTGGAGCCGAGCTCAAGATCTGGCCGCTTCAAGGTGCACTG 180
QY 91 ArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 110
Db 181 CGGAGAGCAGCACTTACTACACAGACCAAGTGTGCGGGTCAAGATCATGTCAC 240
QY 111 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnLeuGlnPro 130
Db 241 CCACAGTCTTACACCGCCAGATCGAGCGGACATCGCCCTGCTGAGCTGGAGAGCGC 300
QY 131 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThrPhePro 150
Db 301 GTAAAGTCTCCAGCCAGTCCACAGGTCACTGCCCCCTGCTCAGAGACTTCCCC 360

```


Db 286 CAGCTTCCGGGTGACGCTTCTGAGCAGTATCTTACTATGGGAGCAGCTCTCTCT 345
Qy 104 ValSerArgIleIleValHisProGlnPheTyrIleGlnThrGlyAlaSerIleAla 123
Db 346 TTGAACCGGATCGGTGGACCCCACTTATACAGGGCCGAGGTGGGAGACGTTGGC 405
Qy 124 LeuLeuGluLeuGluGluProValaenIleSerSerArgValHisThrValMetLeuPro 143
Db 406 CTGCTGAGGCTTGAAGTCTCTGAAATGCTCCACCAATATCCACCCCATATCCCTGGCC 465
Qy 144 ProAlaSerGluThrPheProGlyMetProCysThrValThrGlyTyrPglAspVal 163
Db 466 CTGCTCGGAGACCTTCCCTCGGAGACATCTGCTGGGTGACAGGCTGGGGCGACAT 525
Qy 164 AspAsnAspGluProLeuProProPheProLeuGlyGlnValLysValProIleMet 183
Db 526 GATATATAGACAGGCTCTCCACCTCTATCTCTGAGAGAAATGAAGTTCCATTTGG 585
Qy 184 GluAsnHisIleLeuAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArg 203
Db 586 GAAACAGCCTGTGTACCGGAATACCACTGGCTCTACACGGGAGATGATTTTCCC 645
Qy 204 IleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCysLysGlyAsp 223
Db 646 ATTGTCCATGATGGCATGCTGTGTCTGAAATACAGAGAGACTCTGCGCCAGGCGCAT 705
Qy 224 SerGlyGlyProLeuValCysLysValaenGlyThrTyrLeuGlnAlaGlyValaSer 243
Db 706 TCAGGGGGGCGCATGCTGTCAAAAGTAAGGTACCTGGCTGCAAGGAGGTGTCAGC 765
Qy 244 TTPAspGluGlyCysAlaGlnProAsnArgProGlyTyrThrArgValThrTyrTyr 263
Db 766 TGGGTGAGGGCTGACCAAGCCCAACAGCCCTGGCATACACCGGGTGAATATCTAC 825
Qy 264 LeuAspTyrIleHisThrValProLys 273
Db 826 TTGACTGATCCACCGCTATGTCTCTGAG 855

RESULT 15
US-08-845-998-3
Sequence 3, Application US/08845998
Patent No. 5879892
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P. C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845, 998
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 8..577
US-08-845-998-3

Alignment Scores:
Pred. No.: 8..51e-113 Length: 2259
Score: 1118..50 Matches: 236
Percent Similarity: 41.68% Conservative: 17
Best Local Similarity: 38.88% Mismatches: 22
Query Match: 73.97% Indels: 333
DB: 2 Gaps: 2

US-09-598-982c-52 (1-275) x US-08-845-998-3 (1-2259)

Qy 1 MetLeuSerLeuLeuLeuAlaLeuProValIleAlaSerArgAlaTyrAlaAlaPro 20
Db 8 ATGTGAGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
Qy 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlnGlnAlaProArgSer 40
Db 68 GCCCAAGCCAGGCGCTGTCAGCAACCGGCATTTGGGGGGGCGAGAGCCGCCAGAGC 127
Qy 41 LysTyrProTyrGlnValSerLeuArgValArgAspArgTyrTyrMetHisPheCysGly 60
Db 128 AAGTGGCCCTGCGAGGTAGCTGAGAGTCCGGCCCATCTGATGATCATTCTGCGGG 187
Qy 61 GlySerLeuIleHisProGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
Db 188 GGGCTCCCTCATCCACCCCAAGTGGGTGTAAACCGCGGCGACCTGCGAACCAGCAATC 247
Qy 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGln 100
Db 248 AAGGATCTGGCGCGCTTCAAGGTGCACTGCGGAGACGACACTTACTACAGGACCG 307
Qy 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleGlnThrGlyAla 120
Db 308 CTGCTGCGGTGACAGGATCATCTGCAACCAAGTTCTATCATCATCAGACCGGGCG 367
Qy 121 AspIleAlaLeuLeuGluLeuGluProValaenIleSerSerArgValHisThrVal 140
Db 368 GACATCGCCCTGCTGAGCTGAGGAGCCCGTGAACATCTCCAGCACATCCACAGGTC 427
Qy 141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTyrValThrGlyTyr 160
Db 428 ACGCTGCCCTGCTGCTGAGACCTTCCCTCCGGGAGTCCGTGTGGGTCACTGGCTGG 487
Qy 161 GlyAspValAspAsnAsp----- 166
Db 488 GGCGACGTGACAAATTA-TGGTGGGTGTGGGAGACAGCGGAGGCGCGGCGAGTGGCA 546
Qy 166 ----- 166
Db 547 CCAGTACAGCCACAGCCAGCTCGTGGGTGACAGGTTCCCTCAGGGCGCTCAGGGA 606
Qy 166 ----- 166
Db 607 GGGGGACTGTGAGGCCAGATGATGAGACAGCGGTGGGAGAGGAGGAGAGTGCCT 666
Qy 166 ----- 166
Db 667 GAGCAGACGGTGAATCCAAAGGCGCTGGGCGTCCCAACCCAGGGGTTTGAGAGTC 726
Qy 166 ----- 166

DB 727 CCTTAGCACTCCGCTCGGTTTCCCTTGCTGAAGGTGCATCAAAAGTTTAC 786
QY 166 ----- 166
DB 787 GTACAGCACTTGCTATGTGAGAGAGAAATCACAGGGGGTCTTGCTGGAAGAGAGAGA 846
QY 166 ----- 166
DB 847 CCGGTGCTGGATGAGACCTGCTGCTCCATCCCTGTGTACAGACAGGACAGGGGCC 906
QY 166 ----- 166
DB 907 TGGGAATGGGGTGGTGGCAGTGTGTGGGGGGCTGAGAGAGCTCACTGTGGCCCTCCA 966
QY 166 ----- 166
DB 967 CGAGGCACTTTTCACTTACAGAGTCTGTCCCCATTATTCACAATTACAGACAA 1026
QY 166 ----- 166
DB 1027 GCTTGGGGTACAGCCTGACGCAACCTGGGCTGTGACCTTGGGTCACTCCAGAGGGG 1086
QY 166 ----- 166
DB 1087 CCTGAGCACTGTCCCGCTATTCCGCCCAACAGCGGGAACTGAGCCCAAGCCCTG 1146
QY 166 ----- 166
DB 1147 TGTTCCTCGGCTAGGGCAACGTGAGCATGGGCTAGGCCAGAGAAAGTCAGCTG 1206
QY 167 ----- 168
DB 1207 AGCCAGGGGAGACAGGCTGCGGCTGTCACCCCGTGATGAGGCCAGCTTGGCA 1266
QY 168 ----- 168
DB 1267 ACCTCAGGGGCTCCCTCCCTTCCCAAGTGGGCTTAAATGAGCCAGGACCCAGG 1326
QY 168 ----- 168
DB 1327 ACCAGCTCAGCGAGGGGCTGACTGATTACCGCCCTTCCCGGGGCTGCAGGCA 1386
QY 168 ----- 168
DB 1387 CAGAACAGCACTGGGCCCATGTGTCATCTCCCTGCGGTGACTGTGCACCAAGTCCA 1446
QY 168 ----- 168
DB 1447 CGAAGCAGACCCAGCGGCCCCAGACCGGCTCCACGCCCTCCGCCCCCAAGTGCA 1506
QY 169 LeuProProPhoProLeuLysGlnValLysValProIleMetGlnAsnHisIleCys 188
DB 1507 CTGCGCGCGGCATACCGGCTGAAGAGGTGGAAGTCCCGTAGTGGAACCAACCTTTGC 1566
QY 189 AspAlaLysTyrHisLeuGlnValaTyrThrGlyAspAspValArgIleIleArgAspAsp 208
DB 1567 AACGGGGAATATCACACCGGCTCCATACGGGCAAGCTTCAATCTCCGCGATGAC 1626
QY 209 MetLeuGlyValIleAspSerGlnArgAspSerCysLysGlnValProIleLeu 228
DB 1627 ATGCTGTGTGCGGGAGCGAAATATCACGACTCTGCGAGGTGACTGTGAGGGGCCCTG 1686
QY 229 ValCysLysValAsnGlyThrTrpLeuGlnIleValValSerTrpAspGlnGlyCys 248
DB 1687 GTCTGAAGGTGATGGACCTAACTGCAAGCGGCGGTGTGCTGAGCTGGAGAGAGCTGT 1746
QY 249 AlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHis 268
DB 1747 GCCCAGGCCCAACCGGCTGCACTTAACCCGTGTCACTACTGACTGTGATCCAC 1806
QY 269 HisTyrValProLysLysPro 275
|||||

DB 1807 CACTATGTCCCAAGAGGCC 1827

Search completed: August 27, 2005, 23:44:31
Job time : 194 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2005, 16:09:21 ; Search time 6409 Seconds
(without alignments)
254.007 Million cell updates/sec

Title: US-09-598-982C-52
Perfect score: 1512
Sequence: 1 MSLSLLLALPVLASRAVAAP.....ITRTVTYLLDHHVPRKPP 275

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2.1/USPTO.spool.p/US09598982/rnat.29082005.080947.26125/app_query.fasta_1.455.
-DB=N_Geneseq_16Dec04 -QFMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=prtc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982 @CGN 1_1_708 @runat.29082005.080947.26125 -NCPU=6 -ICPU=3
-NO WMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGCLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001as:*
5: geneeqn2001bs:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004as:*
13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1512	100.0	1154	2	AAV44328
2	1512	100.0	1154	2	AAV42710
3	1512	100.0	1154	3	AAa34959
4	1512	100.0	1154	3	AAf21081
5	1512	100.0	1154	10	ABz96775

6	1512	100.0	1154	10	ADK52587	Adk52587 Hematolog
7	1512	100.0	1154	11	ABD20624	Abd20624 Human pul
8	1512	100.0	1158	9	ACH04035	ACH04035 Human CDN
9	1512	100.0	1158	12	ADP10384	Adp10384 Reference
10	1512	100.0	1158	13	ADP56069	Adp56069 Human PRO
11	1512	100.0	17133	3	AAA34962	Aaa34962 Human ade
12	1512	100.0	17133	3	AAf21084	Aaf21084 Human low
13	1512	100.0	17133	10	ABz96778	Abz96778 Human nuc
14	1512	100.0	17133	10	ABD20627	Abd20627 Human pul
15	1512	100.0	17133	13	ADQ85402	Adq85402 Human tum
16	1430	94.6	1142	13	ADQ85402	Adq85402 Human sof
17	1405	92.9	1143	3	AAA34955	Aaa34955 Human ade
18	1405	92.9	1143	3	AAf21077	Aaf21077 Human low
19	1405	92.9	1143	10	ABz96771	Abz96771 Human nuc
20	1405	92.9	1143	10	ADK52589	Adk52589 Hematolog
21	1405	92.9	1143	11	ABD20620	Abd20620 Human pul
22	1405	92.9	1143	12	ADQ6120	Adq6120 Human olf
23	1405	92.9	1145	3	AAA34956	Aaa34956 Human ade
24	1405	92.9	1145	3	AAf21078	Aaf21078 Human low
25	1405	92.9	1145	10	ABz96772	Abz96772 Human nuc
26	1405	92.9	1145	10	ADJ94865	Adj94865 Novel NOV
27	1405	92.9	1145	11	ABD20621	Abd20621 Human pul
28	1405	92.9	1145	11	ADJ61642	Adj61642 Conceteme
29	1405	92.9	1137	2	AAV44329	Aav44329 Human mas
30	1402	92.7	1137	2	AAV44329	Aav44329 Human mas
31	1402	92.7	1137	2	AAV44329	Aav44329 Human mas
32	1402	92.7	1137	2	AAV44329	Aav44329 Human mas
33	1402	92.7	1137	2	AAV44329	Aav44329 Human mas
34	1402	92.7	1137	2	AAV44329	Aav44329 Human mas
35	1402	92.7	1137	11	ABD20622	Abd20622 Human pul
36	1401	92.7	2662	6	AAAD23854	Aaad23854 Human pro
37	1400	92.6	1128	2	AAV44330	Aav44330 Human mas
38	1394	92.6	1081	2	AAV44331	Aav44331 Human mas
39	1394	92.2	1081	2	AAV44331	Aav44331 Human mas
40	1394	92.2	1081	2	AAV44331	Aav44331 Human mas
41	1394	92.2	1081	3	AAA34960	Aaa34960 Human ade
42	1394	92.2	1081	3	AAf21082	Aaf21082 Human low
43	1394	92.2	1081	6	ABL62377	AbL62377 Colon ade
44	1394	92.2	1081	6	ABL62377	AbL62377 Lung can
45	1394	92.2	1081	6	ABL61818	AbL61818 Colon ade

ALIGNMENTS

RESULT 1	AAV44328	standard; DNA; 1154 BP.
ID	AAV44328	
XX	AAV44328;	
AC		
XX		
DT	24-NOV-1998	(first entry)
XX		
DE	Human mast cell tryptase alpha nucleic acid sequence.	
XX		
KW	Mast cell tryptase alpha; human; MCP-7; mast cell protease 7; blood clot;	
KW	anticoagulant; myocardial infarction; reocclusion; thromboembolism;	
KW	cerebral embolism; thrombosis; therapy; ss.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	18..845
FT		/*tag= a
XX		
PN	WO9824886-A1.	
XX		
PD	11-JUN-1998.	
XX		
PF	25-NOV-1997;	97WO-US021620.
XX		
PR	04-DEC-1996;	96US-0032354P.
XX		
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.	

XX Stevens RL;
 PI WPI: 1998-333308/29.
 XX P-P-SDB; AAM64237.
 DR
 XX
 PT New compositions containing tryptase-7, e.g. mouse mast cell protease-7 -
 PT are used to treat clot formation in e.g. myocardial infarction,
 PT reocclusion following angioplasty or pulmonary thrombo-embolism.
 XX
 PS Disclosure; Page 63; 92pp; English.
 XX
 CC This nucleotide sequence includes a coding region for human mast cell
 CC tryptase alpha (see AAM64237). The invention provides: compositions
 CC comprising an isolated tryptase-7 that may include chimeric proteins that
 CC contain (a) a human tryptase for all but the active site region and (b)
 CC the substrate-binding pocket of mouse tryptase-7 or its homologues (see
 CC AAM64233-36); a method for treating a blood clot by administering a
 CC nucleic acid molecule that codes for a tryptase-7, or an expression
 CC product, to decrease fibrinogen activity; a nucleic acid encoding a
 CC serine protease (SP); and a method of producing a mature SP by expressing
 CC the inactive zymogen in a host cell, and cleaving the enterokinase
 CC susceptibility domain. The tryptase-7 polypeptides can be used to treat
 CC disorders mediated by undesirable thrombus clot formation such as
 CC myocardial infarction and reocclusion following angioplasty of blood
 CC clots associated with pulmonary thromboembolism, deep vein thrombosis,
 CC cerebral embolism, renal vein and peripheral arterial thrombosis. They
 CC are also useful for all surgical procedures that require decreased blood
 CC clots
 XX
 SQ Sequence 1154 BP; 203 A; 411 C; 330 G; 210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5,18e-129 Length: 1154
 Score: 1512.00 Matches: 275
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-598-982c-52 (1-275) x AAV44328 (1-1154)

QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaPro 20
 DB 18 ATGCTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 77
 QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyTlleValGlyGlnGlnAlaProArgSer 40
 DB 78 GCCCGAGTCCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 137
 QY 41 LysTirProTirPglValSerLeuArgValArgAspArgTyrTirPmeHisPheCysGly 60
 DB 138 AAGTGGCCCTGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197
 QY 61 GlySerLeuLeuHisProGlnTirPValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
 DB 198 GGCTCCCTCATCCACCCCGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
 QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGln 100
 DB 258 AAGGAGTCTGGCCAGCTCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317
 QY 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrTlleIleGlnThrGlyAla 120
 DB 318 CTGCTCGAGTCAAGGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 377
 QY 121 AspIleAlaLeuLeuGlnGlnGlnGlnProValAsnIleSerSerArgValHisThrVal 140
 DB 378 GATATGCGCCCTGCTGAGCTGCTGAGGAGCCGTGAATCTCCAGCGCGCTCCACAGCTC 437
 QY 141 MetLeuProProAlaSerGlnTirPheProProGlnMetProCysTyrValThrGlyTirP 160
 DB 438 ATGCTGCCCCCTGCTGAGAGCTTCCCGCGGAGATGCCGTGGGTCACTGGCTGG 497

QY 161 GlyAspValAspAsnAspGluProLeuProProPheProLeuLeuValGlnVal 180
 DB 498 GCGAGTGTGGCAAAAGATGAGCCCTCCACCGGCATTTCCTGAGAGAGTGAAGTTC 557
 QY 181 ProIleMetGluAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
 DB 558 CCCATAATGGAAGAAACCAATTTGTGACCAAAATTCACCTTGGGCGCTTACACGGGAAC 617
 QY 201 AspValArgIleIleArgAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
 DB 618 GACGTCCGCATATCCGTGACACATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
 QY 221 LysGlyAspSerGlyGlyProLeuValCysLysValaGnglyThrTirPLeuGlnAlaGly 240
 DB 678 AAGGCGCACTCGAGAGGCGCCCTGGTGTGCAAGTGATGGCAGCTGCTACAGCGGAGC 737
 QY 241 ValValSerTirPAspGlnGlyCysAlaGlnProAlaGlyTirPLeuGlnAlaGly 260
 DB 738 GTGGTCAAGTGGAGAGAGGCTGTGCCAGCCCAACCGCGCATCTACACCGGTGTC 797
 QY 261 ThrTyrTyrLeuAspTirPleHisIleTyrValProLysLysPro 275
 DB 798 ACTTACTTGTGACTGATCCACCACTATGTCCCAAAAAGCCG 842
 RESULT 2
 AAV42710
 ID AAV42710 standard; cDNA; 1154 BP.
 XX
 AC AAV42710;
 XX
 DT 27-OCT-1998 (first entry)
 XX
 DE Human mast cell tryptase alpha encoding cDNA.
 XX
 KW Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
 KW tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
 KW antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
 KW hyperproliferative skin disease; peptic ulcer; hypersensitiveness;
 KW inflammatory skin condition; human; mast cell tryptase alpha; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 18..845
 FT /*tag= a
 FT /*product= "Human mast cell tryptase alpha"
 FT
 PN MO9833812-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98MO-US001865.
 XX
 PR 05-FEB-1997; 97US-0037090P.
 XX
 PA (BGMH) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Stevens RL, Huang C;
 XX
 DR WPI: 1998-437390/37.
 DR P-P-SDB; AAM63173.
 XX
 PT Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated
 PT inflammatory disorders e.g. asthma.
 XX
 PS Disclosure; Page 44-45; 69pp; English.
 XX
 CC This cDNA encodes the human mast cell tryptase alpha which is a homologue
 CC of the mouse mast cell protease (mMCP-6) zymogen. The invention provides
 CC sequences shown in AAM63160 to AAM63169 that are inhibitors of mMCP-6.
 CC These peptides which are tryptase-6 complex inhibitors, can be used for
 CC treating a mast cell-mediated inflammatory disorder. The inhibitors can

CC be used to treat inflammatory disorders including asthma, allergic
CC rhinitis, urticaria and antioedema, eczematous dermatitis (atopic
CC dermatitis), anaphylaxis, hyperproliferative skin disease, peptic ulcers
CC inflammatory bowel disorder, hyperresponsiveness and inflammatory skin
CC conditions

SQ Sequence 1154 BP; 203 A; 411 C; 330 G; 210 T; 0 U; 0 Other;

Alignment Scores:		
Pred. No.:	5,18e-129	Length: 1154
Score:	1532.00	Matches: 275
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	2	Gaps: 0
US-09-5598-982C-52 (1-275) x AAV42710 (1-1154)		

OY	1	MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaAlaPro	20
Db	18	ATGCTAGACCTGCTGCTGCTGCGCTGCCCTCTCGGCGAGCGCGCCCTACCGCGCCCT	77
OY	21	AlaProValGlnAlaLeuGlnGlnAlaGlyIleValaGlyGlnGlnAlaProArgSer	40
Db	78	GCCCCAATCCAGGCCCTCGACGCAAGCGGGTATGCTGGGGGGTTCAGAGGCCCCCAAGAGC	13
OY	41	LeuTyrProTyrGlnValSerLeuArgValaArgAspArgTyrTyrMetHisPheCysGly	60
Db	138	AAGGAGCCCTGGGAGGAGGACCTGAAAGTCCGGGACCGGATACGTGATGACATCTTCGGGG	197
OY	61	GlySerLeuLeuHisProGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspVal	80
Db	198	GAGCTCCCTCATCCACCCCGAGTGGTGTGACCGCGCGGACACTGGCTGGAGCCGGAATCTC	25
OY	81	LysAspLeuAlaThrLeuArgValaGlnLeuArgGlyGlnHisLeuTyrTyrGlnAspGln	100
Db	258	AAGGATCTGGGCACCCCTCAGGGTGCAACTGCGGGAGCACACCTCTACTACAGGACGAG	31
OY	101	LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla	120
Db	318	CTGCTGCAGCTCAGCAGAGATCATCTGGACCCCAAGATTCATCATCATCCAGCTGGACG	37
OY	121	AspIleAlaLeuLeuGlnLeuGlnGlyProValAspIleSerSerArgValHisThrVal	140
Db	378	GATATCCGCTCGCTGAGAGCTGAGAGAGCCCGGTAAACATTCACAGCGCGTCCACACGCTC	43
OY	141	MetLeuProProAlaSerGlnThrThrPheProGlyMetProCysTyrValThrGlyTyr	160
Db	438	ATGCTGCCCCCTGGCTCGAGACCTTCCCCCGGGAGATCGGCTGGGTCACTGGCTGG	49
OY	161	GlyAspValAspAsnAspGlyProLeuProProProPheProLeuLeuAspGlnAlaVal	180
Db	498	GGCATATGTGACATGATGAGCCCTCCCAACCCCAATTCCTCCGTAAGCAGGTGAAGGCTC	55
OY	181	ProIleMetGluAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp	200
Db	558	CCCATTAATGGAAACCAACATTGTGACGCAAAATACACACTTGGGGCCCTACACGGGAGAC	61
OY	201	AspValArgIleIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys	220
Db	618	GACCTCGGCATCATCCGTGACGACATGCTGTGGCCGGGAACGACAGCGAGGACCTCTGC	67
OY	221	LysGlyLysAspSerGlyGlyProLeuValCysLysValAsnGlyThrTyrLeuGlnAlaGly	240
Db	678	AAGGCGCACCTCTGAGAGGAGCCCTGAGTGTGCAAGGTAAAGGACACCTGGCTCAAGCGCGAGC	73
OY	241	ValValSerTyrAspArgGlyGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgVal	260
Db	738	GTGGTCAAGCTGGAGCGAGGGCTGTGGCCCAACCCAAACCGGCTGGCATCTACACCCGTGTC	79
OY	261	ThrTyrTyrLeuAspTyrPheHisTyrValProLysLysPro	275
Db	798	ACCTACTACTTGGACTGGAATCCACACTAATGCTCCAAAAAAGCGG	842

RESULT 3
AAA34959
ID AAA34959 standard; DNA; 1154 BP.

DT 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2648.

Human, adenosine receptor; low adenosine arisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN W0200009525-A2.

PD 24-FEB-2000.

PF 03-AUG-1999; 99WO-US017712.

PR 03-AUG-1998; 98US-0095212P.

PA (UYEC-) UNIV EAST CAROLINA.

NYCE JW;

DR WPI; 2000-205971/18.

23 New antisense oligonucleotides useful for treating e.g. pulmonary
24 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
25 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
26 PT cancers.

PS Disclosure; Page 808-809; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have anti-inflammatory, antiallergic, antiasthmatic, cytosstatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ON reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA3233 to AAA3512 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 195 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 1154 BP; 203 A; 411 C; 330 G; 210 T; 0 U; 0 Other;

Alignment Scores: 5.18e-129 Length: 1154
Pred. No.:

DB: 3 Gaps: 0
US-09-598-982C-52 (1-275) x AAF21081 (1-1154)
QY 1 MetLeuSerLeuLeuLeuAlaLeuProValIleuAlaSerArgAlaTyrAlaAlaPro 20
DB 18 ATGTGAGCTCTGCTGCTGGCGCTGCCGTCTCTGGGAGCGCGCTTACGCGCCCT 77
QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlnGlnAlaProArgSer 40
DB 78 GCCCAGTCCAGGCGCTGCGAGACGGGTATCGTGGGGGTCAAGAGAGCGCCCGAGAGC 137
QY 41 LysTrpProTglnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGly 60
DB 138 AAGTGGCCCTGGCAGGTGAGCTTGAAGAGTCCGGACCGATCTGATGCACTTCTGCGGG 197
QY 61 GlySerLeuIleHisProGlnTrpValIleuThrAlaAlaHisCysLeuGlyProAspVal 80
DB 198 GGCTCCCTCATCCACCCCGAGTGGGTGACCGCGGGGCACTGCTGGAGCCGAGCGTC 257
QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnHisLeuTyrTyrGlnAspGln 100
DB 258 AAGGATCTGGCCACCTCAGGGTGCACCTGCCGAGACACCTCTACTACCGAGACGAG 317
QY 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleGlnThrGlyAla 120
DB 318 CTGCTGCCAGTACGACGATCATCTGTGACCCACAGTTCTTACATATCCAGCTGGAGCG 377
QY 121 AspIleAlaLeuLeuGlnLeuGlnGlnProValIleuSerSerArgValHisThrVal 140
DB 378 GATATCGCCCTGCTGAGCTGGAGAGCCCGTGAACATCTCCAGCGCGGTCCACAGCGGT 437
QY 141 MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTyrValThrGlyTrp 160
DB 438 ATGCTGCCCCCTGCTCGGAGACCTTCCCGCGGGAGTGCCTGTGGGTCACTGCTGG 497
QY 161 GlyAspValAspAspAspGlnProLeuProProProPheProLeuLeuGlnValLysVal 180
DB 498 GCGGATGTGACAAATGATGAGCCCTCCACCGCCATTTCCCTTAAGACAGGTGAAGTC 557
QY 181 ProIleMetGlnAsnHisIleCysAspAlaTyrTyrHisLeuGlyAlaTyrThrGlyAsp 200
DB 558 CCCATTAATGGAACACATTTGTGACGCGAATAATCCACTTGGGCGCTCAACGCGAGAC 617
QY 201 AspValAlaGlnIleIleArgAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
DB 618 GACGTCCCGATCATCTCGTACACCATGTGTGTGCGGGAAACAGCAGGAGCATCTGTC 677
QY 221 LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGly 240
DB 678 AAGGGGAGCTCTGGAGGGCCCTGGTGTGCAAGTGAATGGACCTGGCTACAGCGGGGC 737
QY 241 ValValSerTrpAspGlnGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgVal 260
DB 738 GTGGTCAAGCTGGAGAGAGGGCGTGTGCCAGGCCCAACCGGCTCGGATCAACCGGTGC 797
QY 261 ThrTyrTyrLeuAspTrpIleHisIleTyrValProLysLysPro 275
DB 798 ACCTACTACTGTGACTGATCCACCATATGTCCCCCAAAAGCCG 842

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
OS WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EP1G-) EP1GENESIS PHARM INC.
XX
XX Nye JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
PS Disclosure; SEQ ID NO 12017; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction.
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1154 BP; 203 A; 411 C; 330 G; 210 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5,18e-129 Length: 1154
Score: 1512.00 Matches: 275
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-598-982C-52 (1-275) x AB296775 (1-1154)
QY 1 MetLeuSerLeuLeuLeuAlaLeuProValIleuAlaSerArgAlaTyrAlaAlaPro 20
DB 18 ATGTGAGCTCTGCTGCTGGCGCTGCCGTCTCTGGGAGCGCGCTTACGCGCCCT 77
QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlnGlnAlaProArgSer 40
DB 78 GCCCAGTCCAGGCGCTGCGAGACGGGTATCGTGGGGGTCAAGAGAGCGCCCGAGAGC 137
QY 41 LysTrpProTglnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGly 60
DB 138 AAGTGGCCCTGGCAGGTGAGCTTGAAGAGTCCGGACCGATCTGATGCACTTCTGCGGG 197

QY 61 GlysSerLeuIleHisProGlnTrpValLeuThrAlaIleHisCysLeuGlyProAspVal 80
 DB 198 GGCTCCCTCATCCACCCCGAGTGGTGTGACCGCGCGCCACATGCTGGGACCGGACGTC 257
 QY 81 LysAspLeuAlaThrLeuArgValGlnIleuArgGlnIleHisLeuTyrTyrGlnAspGln 100
 DB 258 AAGGATCTGACCACTCCAGGAGTGCACATGCGGAGACACACATCTACTACACCGACGACG 317
 QY 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120
 DB 318 CTGCTGCCAGTACAGAGATCATCGTGACACCACTTCTACTCATCTCCAGACTGGAGG 377
 QY 121 AspIleAlaLeuLeuGlnIleuGlnIleuProValAsnIleSerSerArgValHisThrVal 140
 DB 378 GATATCGCCCTGTGAGCTGGAGGAGCCCGTGACATCTCCAGCCGCGCTACACAGCGTC 437
 QY 141 MetLeuProProAlaSerGluThrPheProProGlnMetProCysThrValThrGlyTyr 160
 DB 438 ATGCTGCCCTGTGCTGGAGACTTCCCGCGGAGATGCGTGTGGTCACTGGAGTGG 497
 QY 161 GlyAspValAspAsnAspGluProLeuProProProPheProLeuIleGlnValIleVal 180
 DB 498 GGGGATGTGACATATGAGCCCTCCACCGCCATTTCCCTGAGCAGAGTGAAGTC 557
 QY 181 ProIleMetGlnAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
 DB 558 CCATATATGAAAAACCACTTGTGACGCAAAATACCACTTGGCCCTACACGCGGAGAC 617
 QY 201 AspValArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
 DB 618 GAGGTCCGACATCATCGTGACGATGCTGTGCGGAGAACGCCAGAGGACTCTCTG 677
 QY 221 LysGlyAspSerGlyGlyProLeuValCysIleValAsnGlyThrTrpLeuGlnAlaGly 240
 DB 678 AAGGGGACCTCTGAGAGGCCCCGTGTGCAAGTGAATGACACTGGCTACAGCGGGG 737
 QY 241 ValValSerTrpAspGluGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgVal 260
 DB 738 GTGTGACGTGGACACAGAGGCTGTGCCAGCCACCGGCTGGCATCTACACCCCGTGTTC 797
 QY 261 ThrTyrTyrLeuAspTrpIleHisIleTyrValProIleLysAspPro 275
 DB 798 ACCTACTACTGTGACTGTGATCCACACTATGTCCTCCAAAAGCCG 842
 RESULT 6
 ADKS2587
 ID ADKS2587 standard; DNA; 1154 BP.
 XX
 AC ADKS2587;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Hematological disorder associated Gene ID 1847.
 XX
 KW cytostatic; antiamebic; antischistosomal; virucide; hemostatic; nephrotropic;
 KW cytostatic; thrombolytic; antiparasitic; gene therapy;
 KW hematologic disorder; cancer; Sickle Cell Anemia;
 KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;
 KW Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;
 KW transfusion reaction; Erythroblastosis; mechanical trauma;
 KW micro-angiopathic hemolytic anemia; parasite infection; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 18..845
 FT /-tag= a
 XX
 XX MO2003065871-A2.
 XX
 XX 14-AUG-2003.
 PD
 XX
 PF 28-JAN-2003; 2003WO-US002484.

XX 04-FEB-2002; 2002US-0354333P.
 PR 28-FEB-2002; 2002US-0360258P.
 PR 15-MAR-2002; 2002US-0364476P.
 PR 26-APR-2002; 2002US-0375678P.
 PR 06-JUN-2002; 2002US-0386494P.
 PR 24-JUN-2002; 2002US-0390965P.
 PR 28-JUN-2002; 2002US-0392480P.
 PR 03-JUL-2002; 2002US-0394128P.
 PR 31-JUL-2002; 2002US-0399783P.
 PR 13-AUG-2002; 2002US-0403221P.
 PR 30-AUG-2002; 2002US-0407045P.
 PR 25-NOV-2002; 2002US-0429048P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Carrol JM, Healy A, Welch NS, Kelly LM;
 DR WPI, 2003-731464/69.
 DR P-PSDB; ADKS2588.
 XX
 PT Identifying a compound capable of treating a hematologic disorder (e.g.
 PT anemia or leukemia) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 131,148, 199 or 12303
 PT polypeptide or nucleic acid.
 PS
 PS Disclosure; SEQ ID NO 45; 232pp; English.
 XX
 CC The invention relates to a method of identifying a compound capable of
 CC treating a hematologic disorder comprises assaying the ability of the
 CC compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677,
 CC 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
 CC 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic
 CC acid expression or polypeptide activity, thus, identifying a compound
 CC capable of treating a hematologic disorder. The methods are useful in
 CC diagnosing, preventing and treating hematological disorders, such as
 CC cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia,
 CC Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders
 CC associated with an increased risk of Thrombosis, Herpes, Thalassemia,
 CC antibody-mediated disorders such as transfusion reactions and
 CC Erythroblastosis, mechanical trauma to red blood cells such as micro-
 CC angiopathic hemolytic anemias, infections by parasites or chemical
 CC injuries. The methods may also be used for identifying compounds that
 CC modulate hematological disorders. This sequence corresponds to one of the
 CC genes modulated the compound.
 CC
 XX
 SQ Sequence 1154 BP; 203 A; 411 C; 330 G; 210 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,18e-129 Length: 1154
 Score: 1512.00 Matches: 275
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-598-982C-52 (1-275) x ADKS2587 (1-1154)
 QY 1 MetLeuSerLeuLeuLeuAlaLeuProValIleuAlaSerArgAlaTyrAlaIlePro 20
 DB 18 ATGCTGAGGCTCTGCTGCTGCGCTGCCGCTCTGGGAGCGGCGCTTACCGGCCCCCT 77
 QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlnGlnAlaProArgSer 40
 DB 78 GCCCCAGTCCAGCCCTGTGAGCAACGGGTATCGTCGGGGGTCAAGAGGCCCGCCAGAGC 137
 QY 41 LysTrpProTrpGlnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGly 60
 DB 138 AAGTGCCCTGTGACAGTGTGAGTGCAGATCCGACCAATATCTGATGACATCTTGGCGG 197
 QY 61 GlysSerLeuIleHisProGlnTrpValLeuThrAlaIleHisCysLeuGlyProAspVal 80
 DB 198 GGCTCCCTCATCCACCCCGAGTGGTGTGACCGCGCGCCACATGCTGGGACCGGACGTC 257

QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnHisLeuTyrTrpGlnAspGln 100
DB 258 AAGGATCTGGCCACCTTCAGGGTGAACCTCGGAGACACCTTACTACCAAGAACAG 317
QY 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleGlnThrGlyAla 120
DB 318 CTGCTGCCAGTACAGATCATCTGTGACCCACAGTTTACTATCATCTCAGCTGAGCG 377
QY 121 AspIleAlaLeuLeuGlnLeuGlnGlnProValAsnIleSerSerArgValHisThrVal 140
DB 378 GATATGCGCCCTCTGAGCTGAGAGAGCCCGAATCTTCAGCGCGTCCACAGCGTC 437
QY 141 MetLeuProProAlaSerGlnThrPheProProGlyPheProGlyTyrValThrGlyTyr 160
DB 438 ATGCTGCCCCCTGCTCGAGACCTTCCCCCGGAGATGCTGCTGAGCTGCTGCTGCTG 497
QY 161 GlyAspValAspAsnAspGlnProLeuProProPheProLeuGlnValIleVal 180
DB 498 GCGGATGTGACAAATGATGAGCCCTCCACCGCATTTCCCTGAGCAGGTGAAGTTC 557
QY 181 ProIleMetGluAsnHisIleCysAspAlaIleTyrHisLeuGlyAlaTyrThrGlyAsp 200
DB 558 CCCATATATGAAACACCATTTGTGACGCAAAATACACCTTGGCGCTTACACAGGAGAC 617
QY 201 AspValAlaGlyIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnAspSerCys 220
DB 618 GACGTCCTGATCATCTGTGACACATGCTGTGTGCGGAGAACAGAGGAGGATCTGTC 677
QY 221 LysGlyAspSerGlyGlyProLeuValCysIleValAsnGlyThrTyrLeuGlnAlaGly 240
DB 678 AAGGCGGACTCTGAGAGGCGCTGTGTGACAGTGAATGACCTGTGCTACAGCGGCGC 737
QY 241 ValValSerTyrAspGlnGlyCysAlaGlnProAsnArgProGlyTyrIleTyrThrArgVal 260
DB 738 GTGCTCAGCTGGAGAGAGGCTGTGCTGCCACCAACCGGCTGGATCTACACCGGTGTC 797
QY 261 ThrTyrTyrLeuAspTyrIleHisIleTyrValProIleValSerPro 275
DB 798 ACCTACTACTGTGACTGATTCACCACTATGTCCCCCAAAAGCCG 842
RESULT 7
ABD20624
ID ABD20624 standard, DNA, 1154 BP.
XX
AC ABD20624;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human pulmonary and inflammatory target DNA #235.
XX
KW Human; antitense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasodilation;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIC-G) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahbuddin S;
XX
XX WPI: 2003-093058/08.
DR
XX
XX Pharmaceutical composition for treating asthma, has antitense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 12017; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasodilation,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 1154 BP; 203 A; 411 C; 330 G; 210 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5.18e-129 Length: 1154
Score: 1512.00 Matches: 275
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0
US-09-598-982C-52 (1-275) x ABD20624 (1-1154)
QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaPro 20
DB 18 ATGCTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 77
QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlnGlnAlaProArgSer 40
DB 78 GCCCAGTCCAGGCGCTGACAGAGCGGATGCTGCGGGGTACAGAGGCCCCAGAGAC 137
QY 41 LysTyrProTyrGlnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGly 60
DB 138 AAGTGGCCCTGCGAGAGAGCTGAGAGTCCGACACGATCTGGAAGCATCTTCTGCGGG 197
QY 61 GlySerLeuIleHisProGlnTyrValLeuThrAlaHisCysLeuGlyProAspVal 80
DB 198 GACTCCCTCATCCACCCCACTGGAGTGTGACCCGCGGACATCTCTGGAGCCGAGCTC 257
QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnHisLeuTyrTrpGlnAspGln 100
DB 258 AAGGATCTGGCCACCTTCAGGGTGAACCTCGGAGACACCTTACTACCAAGAACAG 317

Oy	101	LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla	120
Db	318	CTCTCTCCAGTCAGCAGGATCATCTGGACCCACAGTTCTCATCATTCACACGTGGAGCG	377
Oy	121	AspIleAlaLeuLeuGluLeuGluGluProValAsnIleSerSerArgValHisThrVal	140
Db	378	GATATGGCCCTGTGGAGCTGGAGAGAGCCCGTGAACATCTCCAGCCGCTGCACACGGTC	437
Oy	141	MetLeuProProAlaSerGluThrPheProProGlyMetProCysTyrValIleThrGlyTyr	166
Db	438	ATCTGTCCCCCTGCCTCGAGACCTTCCCCCGGGAGATGCGCTGTGGTATCATCGCTGG	497
Oy	161	GlyAspValAspAsnAspGluProLeuProProPheProLeuValGlnValValVal	180
Db	498	GGGAGATGTGGACATATGATGAGCCCTCCACCGGCATTTTCCCTGAAACAGTGAAGTGC	557
Oy	181	ProIleMetGluAsnHisIleCysAspAlaValTyrHisLeuGlyValTyrThrGlyAsp	200
Db	558	CCCATATGGAAAAACACCATTTGTGACGGAAATACACCTTGGGCGCTACACGGAGAC	617
Oy	201	AspValArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys	220
Db	618	GAGCTCCGATCATCTCGTACGACATCGCTGTGTGCGGGAACAGCAGAGGAGCTCTGCG	677
Oy	221	IysGlyAspSerGlyGlyProLeuValCysIysValAsnGlyThrTyrLeuGlnAlaGly	240
Db	678	AAGGGGACACTGGAGAGGCCCTCGGTGTGCAAGGAATGGACCTGGCTTACAGCGGGC	737
Oy	241	ValValSerTyrAspGlyGlyCysAlaGlnProAsnAspProGlyIleSerTyrThrArgVal	260
Db	738	GTCGTCACTGGGACAGAGGCTGTGTGCCAGCCCAACCGCTCGGATCTTACACCCGTGC	797
Oy	261	ThrTyrTyrLeuAspTyrIleHisHisTyrValProIysValysPhe	275
Db	798	ACCTACTACTTGACTGATGCATCCACCACTATGTGCCCAAAAAGCCG 842	

RESULT 8
 ACH04035
 ID ACH04035 standard; cDNA; 1158 BP.
 AC ACH04035;
 XX
 DT 26-SEP-2003 (first entry)
 XX
 DE Human cDNA differentially expressed in lung cancer #240.
 XX
 KW Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;
 XX respiratory disorder; lung cancer; asthma; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003065157-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 04-APR-2002; 2002US-00116802.
 XX
 PR 04-APR-2001; 2001US-0281593P.
 XX
 PA (LASEK/) LASEK A W.
 XX
 PI Lasek AW;
 DR
 WP1; 2003-540803/5.;
 XX
 PT New combination comprising cDNAs that are differentially expressed in
 XX respiratory disorders, useful for diagnosing or treating respiratory
 PT disorders e.g., lung cancer, chronic obstructive pulmonary disease,
 XX emphysema or asthma.
 XX
 PS Claim 1; Page; 39pp; English.

CC The invention relates to a combination comprising cDNAs or their
CC complements that are differentially expressed in respiratory disorder.
CC The combination is useful for preparing a composition for diagnosing or
CC treating respiratory disorders e.g. lung cancer, chronic obstructive
CC pulmonary disease, emphysema or asthma. The present sequence represents
CC human cDNA differentially expressed during lung cancer

Sequence 1158 BP; 203 A; 413 C; 332 G; 210 T; 0 U; 0 Other;

Alignment Scores:

Score:	1512.00	Matches:	275
--------	---------	----------	-----

```
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
```

query match:	100.00%
DB:	9

IRS-09-598-982C-52 (1-275) x ACHC

1 Mett, enSert, enT, enU, enV] at, enPro

db

18 ATTGCTGTAGCCATTGGCTTGCACCGTCATTGGCAGATCCGCCCTACCGGCGCCCT 77

Abstract

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

4. The E-mail address of the author is: maria.maria@univie.ac.at.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

100

UD 318 C1G1GCCCCAG1CAGCAGGAG1CAG1G1GCCCCCAGG11C1GACAG1CAG1CCAGGAC1GGAGCC

121 ASPILEAULEUGIUGIPIOVAIBNIIESEISEALIGVAINISIILVAL 13

DB 3/8 GATATCGCCCTGCTGGAGCTGGAGGAGCCCGTGAACATCTCCAGCCGGLCCACACGGL 42

141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysIrrValIntGlyIrr 16

Db 438 ATGCTGCCCCCTGCTCGGAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGG 439

161 GlyaspvalAspnasnspGluProleuProprophneProleuLysGlnValLysVal

Db 498 GCGATGTGACATGATGAGCCCTCCACCGCCATTTCCTGAAGCAGGTGAAGTC 55

QY 181 ProIleMetGluAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 20

Db 558 CCATATGGAACCACTTTGTGACGCAATACCACTTGGCGCTACACGGAGAC 61

Qy 201 AspValArgIleIleArgAspAspMetLeuCySAIAGIYasNSerGlnArgAspSerCys 22

Db 618 GACGTCGCATCATCCGTGACGACATGCTGTGTGCCGGGAACAGCCAGAGGACTCCTGC 67

221 LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTyrPheGlnAlaGly 24

Db 678 AAGGCGACTCTGAGAGGCCCTGGTGTGCAAGGTGATGGCACCTGGCTACAGCGGCGC 71

241 Val¹Val¹Ser¹Trp¹Asp¹Glu¹Gly¹Val¹Cys¹Ala¹Gln¹Pro¹Asn¹Arg¹Pro¹Gly¹Leu¹Tyr¹Thr¹Arg¹Val¹ 26

Dp 738 GTGCTCAGCTGGACGAGGCTGTGCCACGCCAACCGGCTGGCATCTACACCCGTGC 75

261 ThrIvrvrIeIvAsrrrI]ehIshIstvrVa]ProIvAIvArPro 275

Df 798 ACCGACTGCTGGAGTGCACCACTATGTCCCAAAGGCCG 842

RESULT 9
ADP10384
ID ADP10384 standard; DNA; 1158 BP.
XX
XX ADP10384;
AC
XX
XX 12-AUG-2004 (first entry)
DT
XX
XX Reference mRNA sequences for marker probe #61.
DE
XX transplamt rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; se.
XX
OS Homo sapiens.
PN MO2004042346-A2.
PM
XX 21-MAY-2004.
PD
XX 24-APR-2003; 2003MO-USO12946.
PF
XX 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
RR
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
DR WPI; 2004-400724/37.

Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver pt pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.

Claim 80; SEQ ID NO 393; 1762bp; English.

The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprising detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, CC xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring CC diseases that involve the immune system, e.g. rheumatoid arthritis, CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or CC viral, bacterial or fungal infection. The present sequence represents a mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft rejection and other disorders.

XX
XX Sequence 1158 BP; 203 A; 413 C; 332 G; 210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Score:
5.2e-129	1158	1512.00
Percent Similarity:	Matches:	275
Best Local Similarity:	Conservative:	0
Query Match:	Mismatches:	0
DB:	Indels:	0
	Gaps:	0

US-09-5598-3682-C52 (1-275) x ADP10384 (1-1158)

Df 1 MetheuseerieuleuLeuLeuAlaLeuProValIleuAlaSerArgAlaTyraAlaPro 20

Db 18 ATGCTGAGCGTGCTGCTGGCGGCTGCCGTCCTGCGCAGCGCGGCTTAGCGGCCCT 77

Qy 21 AlAProValGlAlaLeuGlInglInglAlaGlyTYrIvalAlGlylGylngluAlaProArgSer 40

Db	7	GGCCCAAGTCAGAGCCCTGGACGAACCGGGATACGTCGGGGGTCAAGAGAGCCCCAGAGAGC	137
Oy	41	LYSTPPTPTGInValSerLeuArgValAlaArgAspAgtYrTTPmeHisPheCyGly	60
Db	138	AAATGGACCCCTGGCAGGTGAGCTGAGAGTCCGCGACCGATCTGAAATGCACTTCTTGCGGG	197
Oy	61	GLSerLeuIleHisProGlnTrpValLeuThrAlaIleHisCySLeuGlyProAspVal	80
Db	198	GGGCTCCCTCATCCACCCCAATGGGTGCTGACCGGGGCACTGGCTGGAGCCGGAAGTTC	25
Oy	81	LYAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnIleSLeuYrYrGInAspGln	100
Db	258	AAAGATCTGGCCACCTCTCAGGGGTGACATGGGGAGGAGCACTCTACTACAGAGACAG	317
Oy	101	LeuLeuProValSerArgIleIleValHisProGlnPheYrIleIleGlnThrGlyAla	120
Db	318	CTCTCCCTCAGTCAGCAGGATCATCTGTGACCCACCACTTTCTCAATCATCCACACTGGAGCG	377
Oy	121	AspIleAlaLeuLeuGlnLeuGlnIleuProValAsnIleSerSerArgValHisThrVal	140
Db	378	GAAATGCCCCCTGTGGAGCTGGAGGAGCCCGGAACATCTCAGCGGGGTACACAGGTC	437
Oy	141	MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTrpValThrGlyTrp	160
Db	438	ATCTGTCGCCCTGCTCCCGAGAGACTTCCCGGGGAGTGGCTGTGATCATCGGCTGG	497
Oy	161	GlyAspValAlaAspAsnAspGlnIleProLeuProProPheProLeuLYsGlnValIleVal	180
Db	498	GCGGATGTGGACAAATGATGAGGCCCTCCCAACGCAATTCCTCCGGAAGCAGTGAAGGTC	557
Oy	181	ProIleMetGlnAsnHisIleLeuAspAlaIleYrYrHisSLeuGlyAlaIleYrThrGlyAsp	200
Db	558	CCCATATATGAAAAACCACTTTGTGACGCAAAATTCACCTTGGGCGCTTACACGGAGAC	617
Oy	201	AspValArgIleIleArgAspMetLeuCySAlaGlnAsnSerGlnArgAspSerCys	220
Db	618	GAGCTCCGCAATCATCCGTACACACATGCTGTGTGCGGGAAACAGCAGAGGAGATCTCTGC	677
Oy	221	LYsGlyAspSerGlyGlyProLeuValCysIleValAlaGlnYrThrTrpLeuGlnAlaGly	240
Db	678	AAAGGCGAAGCTGGAAGGCGCCCTGGGTGTGCAAGGTGATGGCACTGGCTACAGGCGGGC	737
Oy	241	ValIleSerTrpAspGlnGlyCysAlaGlnProAlaAsnProGlyIleIleYrThrArgVal	260
Db	738	GTGTGAGCTGGGACGAGGGCTGTGCCACGACCCACCGGCTGGCATCTTACACCCGTGC	797
Oy	261	ThrYrTrpLeuAspTrpIleHisIleYrValProLYsLYsPro	275
Db	798	ACCTACTACTGGACTGGATCCACCATATGTCTCCCAAAAGCCG	842
RESULT 10			
ADPS6069			
ID	ADPS6069	standard; cDNA; 1158 BP.	
AC	ADPS6069;		
XX	18-NOV-2004	(first entry)	
XX	Human PRO	cDNA sequence SEQ ID NO:2045.	
DE	human; PRO; immune related disease; inflammatory immune response;		
KW	immune response stimulation; antiinflammatory; antiinfective; antiarthritic;		
KW	antidiabetic; antidiabetic; antiinflammatory; antiproliferative;		
KW	antiproliferative; antiproliferative; CNS; dermatological; gastrointestinal;		
KW	haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;		
KW	neurotrophic; neuroprotective; osteopathic; respiratory; vasotropic;		
KW	vitruide; gene therapy; gene; ss.		
XX	Homo sapiens.		
OS			
PN	WO2004039956-A2.		
XX			
PD	13-MAY-2004		

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2005, 15:02:36 ; Search time 3552 Seconds
(without alignments)
3751.460 Million cell updates/sec

Title: US-09-598-982C-52

Perfect score: 1512
Sequence: 1 MSLILLALPVLASRAVAP.....ITRTVYLDVIMHVPKP 275

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlp
-O=/cn2_1/USPTO.spool.p/US0598982/crunat.29082005.080946.26113/app.query.fasta_1.455
-DB=GenEmbl -QFMT=fastad -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=humano.cdi -LIST=45
-DOALIGN=200 -THR.SCOR=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0598982 @CN 1.1.5600 @runat.29082005.080946.26113 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOBQUERY -NEG.SCOR=0 -WAIT -DSPBLOCK=100 -LONGCLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_pro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1512	100.0	1154	6	AR080459 Sequence
2	1512	100.0	1154	9	HUMTRY M30038 Human trypt
3	1494	98.8	884	9	AF206665 Homo sapi
4	1494	98.8	1206	9	BC028059 Homo sapi

5	1494	98.8	1207	9	BC051852	BC051852 Homo sapi
6	1414	93.5	896	9	BC074975	BC074975 Homo sapi
7	1405	92.5	896	9	BC074974	BC074974 Homo sapi
8	1405	92.9	1143	9	HUMBTRYP	M37488 Human beta-
9	1405	92.9	1145	9	S55551	S55551 beta-trypta
10	1405	92.9	1194	9	BC029356	BC029356 Homo sapi
11	1405	92.9	1235	9	BC038416	BC038416 Homo sapi
12	1405	92.9	1460	9	BC065923	BC065923 Homo sapi
13	1403	92.8	825	9	CR541836	CR541836 Homo sapi
14	1402	92.7	1137	6	AR080460	AR080460 Sequence
15	1402	92.7	1137	6	HUMTRY1A	M33491 Human trypt
16	1401	92.6	2662	6	AX338508	AX338508 Sequence
17	1400	92.6	1128	6	AR080461	AR080461 Sequence
18	1400	92.6	1128	6	HUMTRY2A	M33492 Human trypt
19	1394	92.2	1081	6	AR080462	AR080462 Sequence
20	1394	92.2	1081	6	AR482491	AR482491 Sequence
21	1394	92.2	1081	6	AX329646	AX329646 Sequence
22	1394	92.2	1081	6	AX330205	AX330205 Sequence
23	1394	92.2	1081	6	AX334644	AX334644 Sequence
24	1394	92.2	1081	6	AX375047	AX375047 Sequence
25	1394	92.2	1081	9	HUMTRY3A	M33493 Human trypt
26	1378.5	91.2	768	9	AF206666	AF206666 Homo sapi
27	1364	90.2	1221	6	BD222223	BD222223 Human nuc
28	1364	90.2	1221	6	AX014344	AX014344 Sequence
29	1348	89.2	5441	9	AF098328	AF098328 Homo sapi
30	1290	85.3	735	6	AX347834	AX347834 Sequence
31	1290	85.3	771	6	AX347838	AX347838 Sequence
32	1287	85.1	735	6	AX347881	AX347881 Sequence
33	1287	85.1	735	6	AX347883	AX347883 Sequence
34	1287	85.1	771	6	AX347873	AX347873 Sequence
35	1287	85.1	771	6	AX347875	AX347875 Sequence
36	1284	84.9	735	6	AR165109	AR165109 Sequence
37	1284	84.9	735	6	BD211487	BD211487 Enzymatic
38	1284	84.9	735	6	AX347843	AX347843 Sequence
39	1284	84.9	771	6	AR165112	AR165112 Sequence
40	1284	84.9	771	6	BD211490	BD211490 Enzymatic
41	1284	84.9	771	6	AX347841	AX347841 Sequence
42	1282	84.8	735	6	AX347879	AX347879 Sequence
43	1282	84.8	771	6	AX347871	AX347871 Sequence
44	1281	84.7	735	6	AX347865	AX347865 Sequence
45	1281	84.7	735	6	AX347867	AX347867 Sequence

ALIGNMENTS

RESULT 1	AR080459	1154 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	AR080459	Sequence	11 from patent US 5968782.		
DEFINITION	AR080459				
ACCESSION	AR080459.1	GI:10007194			
VERSION	AR080459.1				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1154)				
AUTHORS	Stevens,R.L.				
TITLE	Mast cell protease that cleaves fibrinogen				
JOURNAL	Patent: US 5968782-A 11 19-OCT-1999;				
FEATURES	Location/Qualifiers				
source	1..1154				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				

Alignment Scores:
Pred. No.: 7.85e-136
Score: 1512.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
Length: 1154
Matches: 275
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-598-982C-52 (1-275) x AR080459 (1-1154)

QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValIleuAlaSerArgAlaTyrAlaIlePro 20
 DB 18 ATGCTAGAGCTGCTGCTGGCGCTGCCGCTCTGGCAGCGCGCCCTACCGGCCCCCT 77

QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValaGlyGlyGlnAlaProArgSer 40
 DB 78 GCCCCAGTCAGAGCCCTGCGAGCAAGCGGGATGTCGGGGGTGAGAGAGGCCCCAGAGAC 137

QY 41 LysTrpProTrpGlnValSerLeuArgValaArgAspArgTyrTrpMetHisPheCysGly 60
 DB 138 AAGTGGCCCTGGAGGTGAGCTGAGAGTCCGAGCCAGTACGATGAGACCTTCTGGCGGG 197

QY 61 GlySerLeuIleHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
 DB 198 GGTCTCCATGACACCCCGAGTGGTGGTGGACCGCGCGGACACTGCTGGAGCCGAGCGTC 257

QY 81 LysAspLeuAlaThrLeuArgValaGlnLeuArgGlyGlnHisLeuTyrTrpGlnAspGln 100
 DB 258 AAGGATCTGGCCACCTCAGGGGTGCAACTGCCGGAGCACACCTCTACTACAGAGACAG 317

QY 101 LeuLeuProValSerArgIleIleValaHisProGlnPheTyrIleIleGlnThrGlyAla 120
 DB 318 CTGCTCCAGTCAAGCAGGATCATCTGACCCACAGTCTTACATCATCAGACTGGAGCG 377

QY 121 AspIleAlaLeuLeuGlnLeuGlnGluProValAsnIleSerSerArgValHisThrVal 140
 DB 378 GATATGCCCTGCTGGAGCTGGAGGAGCCCGTGAACATCTCCAGCGCGCTCCACAGCGTC 437

QY 141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThrGlyTyr 160
 DB 438 ATGCTGCCCCCTGCTCCGAGACCTTCCCCCGGGGATGCCGCTGGCTGCTGCTGCTG 497

QY 161 GlyAspValAspAsnAspGluProLeuProProProPheProLeuLysGlnIleValaVal 180
 DB 498 GGGAGTGTGACATATATAGCCCTCCACCGCATTTTCCCTGAGAGAGGTAAGAGTC 557

QY 181 ProIleMetGlnAsnHisIleCysAspAlaIleTyrHisIleuGlyValaTyrThrGlyAsp 200
 DB 558 CCATATATGGAATAACACATTTGTGACGCAATAACACCTTGGGCGCTTACACAGGAGAC 617

QY 201 AspValaIleGlyIleLeuArgAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
 DB 618 GACGTCCGATCATCTCGTACGACATGCTGTGTGCGGGAGAACGCCAGAGGAGCTCTCC 677

QY 221 LysGlyAspSerGlyGlyProLeuValaCysLysValaAsnGlyThrTrpLeuGlnAlaGly 240
 DB 678 AAGGCGACCTCTGAGAGGCCCTGTGTGTGCAAGGTAAATGGACCTTGGCTACAGCGGAGC 737

QY 241 ValaIleSerTrpAspGlnGlyCysAlaGlnProAsnArgProGlyTyrIleTyrThrArgVal 260
 DB 738 GTGGTACGTGGGAGCAGAGGGCTGTGCCAGGCCAACCGGCGTGGCATCTACACCGGTTC 797

QY 261 ThrTyrTrpLeuAspTrpIleHisHisTyrValaProLysGlyPro 275
 DB 798 ACTTACTACTGTGACTGATCCACCACTATGTCCCAAAAAGCGC 842

RESULT 2
 LOCUS HUMTRY 1154 bp mRNA linear PRI 07-FEB-1996
 DEFINITION Human tryptase mRNA, complete cds.
 ACCESSION M30038
 VERSION M30038.1 GI:1182066
 KEYWORDS serine protease; tryptase.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1154)
 AUTHORS Miller J.S., Westin, E.H. and Schwartz, L.B.
 TITLE Cloning and characterization of complementary DNA for human
 trypase

JOURNAL J. Clin. Invest. 84 (4), 1188-1195 (1989)
 MEDLINE 90009311
 PUBMED 2677049
 REFERENCE 2 (bases 1 to 1154)
 AUTHORS Schwartz, L.B.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-1990) Lawrence B. Schwartz, Medicine, Virginia Commonwealth University, Richmond, VA 23298, USA
 COMMENT On Feb 7, 1996 this sequence version replaced gi:339978.
 FEATURES
 source
 location/Qualifiers
 1..1154
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="lung"
 <1..1154
 /product="TRY mRNA"
 18..845
 /codon_start=1
 /product="trypase precursor"
 /protein_id="AAA86934.1"
 /db_xref="GI:1182067"
 /translation="MLSLLILALPYLASRAAYAAPVQALQAGIVGGQEARPRKWP
 QVSLKVRDYMHEFGGSLHPQWVLAHCLGDPVQDLATLRVQREQHLYQDL
 PVSRIIVHPFYIIQTGADIALLELEEVNIVSSVHTVMLPASPTEPPMPQWTGM
 GDVNDDEPLPPFPFLKQYKVPVIMENHICDARYTGAYGDDVRIRIDMLCAGNSORD
 SCKDGGGFLVCKVNGTWLDAQVVSMDGCAQPNRPGIYRVTYLDWIHHVPRKP"
 18..107
 108..839
 /product="trypase"
 ORIGIN
 Alignment Scores:
 Pred. No.: 7,856-136 Length: 1154
 Score: 1512.00 Matches: 275
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-598-982C-52 (1-275) x HUMTRY (1-1154)

QY 1 MetLeuSerLeuLeuLeuAlaLeuProValIleuAlaSerArgAlaTyrAlaIlePro 20
 DB 18 ATGCTAGAGCTGCTGCTGGCGCTGCCGCTCTGGCAGCGCGCCCTACCGGCCCCCT 77

QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValaGlyGlyGlnAlaProArgSer 40
 DB 78 GCCCCAGTCAGAGCCCTGCGAGCAAGCGGGATGTCGGGGGTGAGAGAGGCCCCAGAGAC 137

QY 41 LysTrpProTrpGlnValSerLeuArgValaArgAspArgTyrTrpMetHisPheCysGly 60
 DB 138 AAGTGGCCCTGGAGGTGAGCTGAGAGTCCGAGCCAGTACGATGAGACCTTCTGGCGGG 197

QY 61 GlySerLeuIleHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
 DB 198 GGTCTCCATGACACCCCGAGTGGTGGTGGACCGCGCGGACACTGCTGGAGCCGAGCGTC 257

QY 81 LysAspLeuAlaThrLeuArgValaGlnLeuArgGlyGlnHisLeuTyrTrpGlnAspGln 100
 DB 258 AAGGATCTGGCCACCTCAGGGGTGCAACTGCCGGAGCACACCTCTACTACAGAGACAG 317

QY 101 LeuLeuProValSerArgIleIleValaHisProGlnPheTyrIleIleGlnThrGlyAla 120
 DB 318 CTGCTCCAGTCAAGCAGGATCATCTGACCCACAGTCTTACATCATCAGACTGGAGCG 377

QY 121 AspIleAlaLeuLeuGlnLeuGlnGluProValAsnIleSerSerArgValHisThrVal 140
 DB 378 GATATGCCCTGCTGGAGCTGGAGGAGCCCGTGAACATCTCCAGCGCGCTCCACAGCGTC 437

QY 141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThrGlyTyr 160

Db	Accession	Version	KeyWords	Source	Organism	Title	Journal	PubMed	Reference	Authors	Journal Title	Features
Db	438	ATGCTGCCCCCTGCTGGAGACCTTCC	CCCCGGGAGATGCCGTCTGGGTCACTGGCTGG	497								
Qy	161	GIYAAPValAlaPanaPAPGluProLeuP	ProPheProPheProLeuValAlaValAl	180								
Db	498	GGCGATGTGGACATGATGAGCCCCCTCC	ACCGCATATTTCCCTGAAGCAGGTGAAGGTC	557								
Qy	181	Pro1LeuMetGluAanHis11LeCysAsp	AlaValPheTyrHisLeuGlyAlaTyrThrGly	200								
Db	558	CCCAATATGAAAAACCAATTGTGACGCA	AAATATACCACTTGGCGCTTAACAGCGAGAC	617								
Qy	201	AspValAlaArg1Le1LeaGAspAspMet	LeuCysAlaGlaValaSenSerGlnArgAsp	220								
Db	618	GACGTCGGCATCATCCGACGACATGTGT	GTGTGTCCGGGAACACGACGAGGATCTCTGC	677								
Qy	221	LysGlyAspSerGlyGlyProLeuValCys	LysValaHengIlyThrTTPLeuGlnAlaGly	240								
Db	678	AAGGCGCAGCTGTGAGGGCCCTCGTGTG	CAAGGTGAATGAGCAGCTGGCTACAGCGGGC	737								
Qy	241	ValValSerTTPAPAGGluGlyCysAlaGln	ProAanArgP-roGly11eTyrThrArgVal	260								
Db	738	GTGTGTACGTGGAGCGAGGGCTGTGGCC	AGCCCAACGGCTGGCATTTACACCGGTGC	797								
Qy	261	ThrTyrTyrLeuAspTTP1eHis1eTyrVal	ProTylsPPro 275									
Db	798	ACCTACTACTTGAAGCTGGATCCACCACT	ATATGTCCCAAAAGCCG 842									
RESULT 3	AF206665											
LOCUS	AF206665	884 bp	mRNA	linear	PRI 24-OCT-2002							
DEFINITION	Homo sapiens mast cell alpha II	tryptase mRNA, complete cds,										
ACCESSION	AF206665											
VERSION	AF206665.1	GI:11493897										
KEYWORDS												
SOURCE												
ORGANISM	Homo sapiens (human)											
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.											
	1 (bases 1 to 884)											
	Wang,H.W., McNeill,H.P., Thomas,P.S., Murphy,B.N., Webster,M.J.,											
	Hettiaratchi,A., King,G., Heywood,G.J., Huang,C., Stevens,R.L. and											
	Hunt,J.E.											
	delta tryptase is expressed in Multiple Human Tissues, and a											
	Recombinant Form Has Proteolytic Activity											
	Submitted (19-NOV-1999) Pathology, University of New South Wales,											
	High St., Kensington, NSW 2052, Australia											
	Location/Qualifiers											
	1..884											
	/organism="Homo sapiens"											
	/mol_type="mRNA"											
	/db_xref="taxon:9606"											
	/chromosome="16"											
	/map="16p13.3"											
	/tissue_type="lung"											
	/clone_lib="Invitrogen cat. number D6090-15"											
	11..838											
	/note="serine protease; alternatively spliced; similar to											
	the product encoded by Genbank											

[illegible]

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	REMARK COMMENT
BC028059 BC028059.1 GI:20380844 MGC.	Homo sapiens Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 1206)			
	Straussberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Bietow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Cabavant, T. L., Scheerz, T. E., Brownstein, M. J., Ustin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullan, S. J., Bosak, S. A., McEwan, P. J., McEwan, R. K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Wolley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hu, Y., Hu, Y., S. W., Villalón, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A. C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Girmwood, J., Schmutz, J., Myers, R. M., Butcherfield, Y. S., Krzywinski, M. I., Skalska, U., Smalls, D. E., Scherch, A., Schein, J. B., Jones, S. J., and Marra, M. A.			
	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
	2 (bases 1 to 1206)			
	Straussberg, R.			
	Direct Submission			
	Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
	NIH-MGC Project URL: http://mgc.nci.nih.gov			
	Contact: MGC help desk			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: Life Technologies, Inc.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),			
	Galtherburg, Maryland;			
	Web site: http://www.nisc.nih.gov/			
	Contact: nisc.mgc@hgrl.nih.gov			
	Ahtler, N., Ayle, K., Beckstrom-Sternberg, S. M., Benjamin, B., Blakesley, R. W., Bouffard, G. G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Haderu, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q. L., Masello, C., Maseri, B., Mastrian, S. D., McCloskey, J. C., McConwell, J., Pearson, R., Stantirlop, S., Thomas, P. J., Touchman, J. W., Targoson, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.			
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov			
	Series: IRAP Plate: 62 Row: E Column: 8			
	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13699841.			
	Location/Qualifiers			
	1..1206			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="MGC:39869 IMAGE:5181815"			
	/tissue_type="Brain, Lung, Testis, adult, pooled whole"			
	/clone_id="NIH MGC_115"			
	/lab_host="DH10B"			
	/note="vector: pCMV-SPORT6"			

gene	1. .1206	/gene="TPS1"	/note="Synonyms: TPS2, alpha IT"
		/db_xref="LocustID:7176"	/db_xref="MIM:191080"
CDS	13. .840	/gene="TPS1"	/codon_start=1
		/product="TPS1 protein"	/protein_id="AAH28059.1"
		/db_xref="GI:20380845"	/db_xref="LocustID:7176"
		/db_xref="MIM:191080"	/translation="MSLLSLALPYLASPAVAAPAPVOALQOAGIVGGQAPSKRMH QYSIRLRDRVMYHPCGGSLIHPOWYIPLAHLGCGVDMLRLVQLRLEGHLYYQDOL PNSRIIVHPQFIYIOTGADIALBELFEPMNISSRVHMLPASEETPPMPCMYG GVDNDNEIPLPPPLKQVAPLMEHNIIDCATYHIGATYGDVRLIRDMICAGNTRR SCQSGSGGPLVCKVNGVTWLQAGVSWDEGCAQPNRPGLYTRVYTYLDM IHHVYPKEK 103. .813
misc_feature		/gene="TPS1"	/note="Tryp. SPC: Region: Trypsin-like serine protease"
		/db_xref="CCD:smart00020"	
ORIGIN			
Alignment Scores:			
Pred. No.:	4,466-134	Length:	1206
Score:	1494.00	Matches:	271
Percent Similarity:	99.64%	Conservative:	3
Best Local Similarity:	98.55%	Mismatches:	1
Query Match:	98.81%	Indels:	0
	9	Gaps:	0
US-09-598-982C-52 (1-275) x BC028059 (1-1206)			
QY	1 MetIeuSerleuIeuIeuIeuIaIeuProValIeuIaSerArgaIaTyrAlaIaPro	20	
Db	13 ATGCTAGAGCTGCTGCTGCTGCGCTGCCCTCTCGCGAGACCGCGCTACGCGCCCT	72	
QY	21 AlaProValGlnAlaIeuGlnGlnAlaGlyIleValGlyGlnGlnAlaProArgSer	40	
Db	73 GCCCCAGTCCAGGCGCTCGACGACAGCGGGTATCGTCGGGGTCAAGAGGCCCAAGAGC	132	
QY	41 LyeTTrProTTrGlnAlaSerIeuIuArgValaArgaPArgTTrTTrMetHisIbPheCysGly	60	
Db	133 AAGTGGCCCTGGAGGTGAGCCTGAGAGTCCGCGACCAATCTGAGATGACCTTGTGGG	192	
QY	61 GlySerIeuIleHisProGlnTTrValIeuThrAlaAlaHisCysIleuGlyProAspVal	80	
Db	193 GGTCTCCCTATCCACCCCGACAGTGGGTGCGAGCCGGGCGACTGCTCGGAGCCGAGCTC	252	
QY	81 LysAspIeuAlaThrIeuIuArgValaGlnIeuIuArgGlnIuIleuIuTyrGlnAspGln	100	
Db	253 AAGATCTGGCCACCTCTGAGGTGCAATCGCGGAGAGACCTCTACTACCAAGACAG	312	
QY	101 LeuIeuProValSerArgIleIleValaHisProGlnPheTyrIleIleGlnThrGlyAla	120	
Db	313 CTGCTGCGGCTACGACGAGATCATCTGTGACCCCAAGTTCATCATCTCAGACTGAGCG	372	
QY	121 AspIleAlaIeuIeuGlnIeuGlnIuProValAsnIleSerSerArgValHisThrVal	140	
Db	373 GATATGCGCTGCTGAGAGCTGAGAGAGCCCGTGAAATCTCCACCGCGTCCACACGGTC	432	
QY	141 MetIeuProValaSerGlnuThrPheProPogIuMetProCysTTrValaThrGlyTTr	160	
Db	433 ATCTGCGCCCTGCTCGGAGACTTCCCGGGGGAAGCGGTGTGGGTACTGGCTGG	492	
QY	161 GlyAspValaAspAsnAspIuProIeuProProPheProIeuIuGlnValaIysVal	180	
Db	493 GGGGATGTGGACATGATGAGCCCGTCCACCGCATTTTCCCTGAGAGCAGGTGAGTGC	552	
QY	181 ProIleMetGlnAsnHisIleCysAspAlaIuTyrHisIleuGlyAlaIuTyrHisGlyAsp	200	
Db	553 CCATATATGGAACCACTTTGTGACGCAAAATTCACCTTGGCGCTACACGGAGAC	612	

QY 141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThrGlyTrp 160
 DB 426 ATGCTGCCCCCTGCTCGAGACCTTCCCCCGGGATGCGGTGCTGCGCTGCTGCTG 485
 QY 161 G1AAspValAspAsnAspGluProLeuProProProPheProLeuLeuValValVal 180
 DB 486 GGGAGATGTGACATATATATAGCCCTCCACCCCACTTCCCTGTAAAGAGGTGAAGTTC 545
 QY 181 Pro11MeGluValAsnHis11LeCysAspAlaValTyRHisLeuGlyVal1aTyRThrGlyAsp 200
 DB 546 CCGATATATGGAACCAACATTTGTGAGCAAAATACCACTTGCCCTTACACGGGAGAC 605
 QY 201 AspValArg11Le11LeArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
 DB 606 GACGTCCGATCATCCGTGACGACATGCTGTGTGCGGGAAACACCCGGAGGACATCATGC 665
 QY 221 LysGlyAspSerGlyValProLeuValCysLysValAsnGlyTyRThrTrpLeuGln1aGly 240
 DB 666 CAGGGGAGCTCTGAGAGGCCCCCTGGTGTGCAAGTAAAGGACCTGGCTACAGGGGGGC 725
 QY 241 ValValSerTrpAspGluGlyCysAlaGlnProAsnArgProGly11LeTyRThrArgVal 260
 DB 726 GTGTGAGCTGGAGACAGGGCTGTGCTGCCAGCCCAACCGGCTTGATCTACACCCGTTC 785
 QY 261 ThrTyRTrpLeuAspTrp11LeHis11TyRValProLysAlaPro 275
 DB 786 ACCTACTACTTGATGATCCACCACTATATGTCCTCCAAAGACCG 830
 RESULT 6
 LOCUS BC074975 896 bp mRNA linear PRI 04-AUG-2004
 DEFINITION Homo sapiens tryptase beta 1, mRNA (cDNA clone MGC:103905
 IMAGE:30915294), complete cds.
 ACCESSION BC074975
 VERSION BC074975.2 GI:50960667
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 896)
 AUTHORS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheefter C.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huix S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whitting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E., Jones S.J. and Marra M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBLISHED 12477932
 REFERENCE 2 (bases 1 to 896)
 AUTHORS Director MGC Project.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Aug 4, 2004 this sequence version replaced gi:49901651.

Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Genome Sequence Centre, British Columbia Cancer Center
 CDNA Library Preparation: British Columbia Cancer Research Center
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Mason, Mike R. Mayo, Josh Moran, Ryan Morin, Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabu, Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska, Duane Smalhus, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRBU Plate: 2 Row: C Column: 7.
 Location/Qualifiers
 1..896
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:103905 IMAGE:30915294"
 /tissue_type="Pooled tissue, PCR rescued clones"
 /clone_lib="NIH MGC 271"
 /note="Vector: pCR4 Topo TA with reversed insert"
 1..896
 /gene="TPSB1"
 /note="synonyms: TPS2, beta 1, tryptase-II, TPS1"
 /db_xref="LocusID:7177"
 /db_xref="MIM:191081"
 34..861
 /gene="TPSB1"
 /codon_start=1
 /product="beta tryptase 1, precursor"
 /protein_id="AAH74975.1"
 /db_xref="GI:50960668"
 /db_xref="LocusID:7177"
 /db_xref="MIM:191081"
 /translation="MLSLLALPYLASRAYAAPQALORVIGVGEPRSKMP
 QVSLRHHVPMNHFCQGSLLHPQWLTAAHCVGPDVLDALRVQLREOHLYDQQL
 FVSRIVHPQVYTDIGASDILIELEEVNVSIVHTLTPASTPSPGMPVWTGW
 GVDVDELPPFPDKQYKVPIMENHICDAKYNIGAYGVDVRIYRDMLCAGTRRD
 SCQDPSGSLVCKNKGWTLQAGVVSWMGCAQPNRPPIYTRVTVYLDWIHHYPRKP"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,586-126 Length: 896
 Score: 1414.00 Matches: 255
 Percent Similarity: 95.27% Conservative: 7
 Best Local Similarity: 92.73% Mismatches: 13
 Query Match: 93.52% Indels: 0
 DB: 9 Gaps: 0
 US-09-598-982c-52 (1-275) x BC074975 (1-896)
 QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyRAlaAlaPro 20
 DB 34 ATGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 93
 QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyTyleValGlyGlnGlnAlaProArgSer 40
 DB 94 GCGCCAGGCGAGGCGCTGCTGAGCGAGTGGCATCTGTGGGGGTCAAGAGCCCGGAGAC 153
 QY 41 LysTrpProTrpGlnValSerLeuArgValAlaArgAspArgTyRTrpMetHisPheCysGly 60
 DB 154 AAGTGGCCCTGGCAGTGAAGCTGAGAGTCCAGCGCCCATGATGATGATGATGATGATG 213
 QY 61 GlySerLeuLeuLeuLeuLeuProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal 80

```

Db      214 GGCCTCCATCCACCCCAAGGGGTGCTGACCGGACGCGACTGCTGGACCGGACTC 273
Oy      81  LysApLeuAlaThrLeuArgValGlnLeuArgGlnHisLeuTyrTyrGlnAspGln 100
Db      274 AAGGATCGCGCGCCCTGAGGATGCACTGGCGGAGACGACCTTACTACAGAGACGAG 333
Oy      101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120
Db      334 CTGCTGCGCGGTACGAGGATCTCTGTGACCCACGATTCACACCGCCAGATCGGAGCG 393
Oy      121 AspIleAlaLeuLeuGlnLeuGlnGluProValAsnIleSerSerArgValHisThrVal 140
Db      394 GACATCGCGCTCTGCTGAGTGGAGACCGGGAACGCTCTCAGCAGCAGTCCACGCGTTC 453
Oy      141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTyrTyrValThrGlyTyr 160
Db      454 ACCCTGCGCCCTGCTCAGAGACCTTCCCGCGGAGATGCCGCTGGGTCACTGGCTGG 513
Oy      161 GlyAspValAspAspAspGluProLeuProProProPheProLeuGlnValValVal 180
Db      514 GCGCGTGTGACAAATGATGAGCGCTCCACCGCATTTCTCTAGACGAGTGAAGGTC 573
Oy      181 ProIleMetGluAsnHisIleCysAspAlaTyrTyrHisLeuGlyAlaTyrThrGlyAsp 200
Db      574 CCCATATGAGAAACCACTTTGTGACCGAAATACACCTTGGCGCTTACACGCGGAGAC 633
Oy      201 AspValArgIleIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspCys 220
Db      634 GACGTCCCGCATGCTCGTGACGACATGCTGTGTGCGCGGACACCGGAGGAGCATCAGTC 693
Oy      221 LysGlyAspSerGlyGlyProLeuValCysIleValAsnGlyTyrThrLeuGlnAlaGly 240
Db      694 CAGGGCGACTCCGAGGGCGCTGTGTGTGCAAGGTAATGACCATGCTGTGACGCGGCG 753
Oy      241 ValValSerTyrAspGluGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgVal 260
Db      754 GTGTGACGCTGGGCGAGGGCTGTGTGCCAGCCCAACCGCGCTGACACCGCTGTTC 813
Oy      261 ThrTyrTyrLeuAspTyrIleHisIleTyrValProValLeuAspPro 275
Db      814 ACCTACTACTTGACTGATCCACCATATGTGCCCAAAAGCCG 858

```

RESULT 7
LOCUS BC074974 896 bp mRNA linear PRI 04-AUG-2004
DEFINITION Homo sapiens tryptase beta 2, mRNA (cDNA clone MGC:104064
IMAGE:30915512), complete cds.
ACCESSION BC074974
VERSION BC074974.2 GI:50959860
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 896)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schmeider, C.M., Schuler, G.D.,
Altshuler, S.L., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Matusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Ueda, T.B., Toshiyuki, S.,
Carinini, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J.,
Abrahamson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunatane, P.H., Richard, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, U., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, J.A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,

TITLE Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 896)
AUTHORS Director MGC Project.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 4, 2004 this sequence version replaced gi:49901868.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
Center
cDNA Library Preparation: British Columbia Cancer Research Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska,
Duane Smallue, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRB Plate: 4 Row: E Column: 9.
Location/Qualifiers

FEATURES

source 1..896
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:104064 IMAGE:30915512"
/tissue_type="Pooled tissue, PCR rescued clones"
/clone_lib="NIH MGC 271"
/note="Vector: pCR4 Topo TA with reversed insert"
1..896
/gene="TPSB2"
/db_xref="LOCUSID:64499"
34..861
/gene="TPSB2"
/product="tryptase beta 2, precursor"
/protein_id="AAH74974.1"
/db_xref="GI:50959861"
/db_xref="LOCUSID:64499"
/translation="MLNLILALPVLASRAVAPQALQRVGIVGGQEARSKWP
QVSLRIGPVWMEHRCGSLIHPOVLAALRAHGVGDVDAALRYOLREOHLYYDOL
PVSIIYHPQYTRQIGADIALLELEPXYKSSVHYVTYTPASETPRCMPQVDTG
GVDVNDLRPEPFKQVPIEMNHICDAKTHIGATYGGDVRIVRDMLCAGTRRD
SCQDSGSLPVCXVNGTWLQAGVVSMEGCAQPNRPGLYTRVYTLDMIHIVPKP"

CDS

gene 1..896
/gene="TPSB2"
/db_xref="LOCUSID:64499"
34..861
/gene="TPSB2"
/product="tryptase beta 2, precursor"
/protein_id="AAH74974.1"
/db_xref="GI:50959861"
/db_xref="LOCUSID:64499"
/translation="MLNLILALPVLASRAVAPQALQRVGIVGGQEARSKWP
QVSLRIGPVWMEHRCGSLIHPOVLAALRAHGVGDVDAALRYOLREOHLYYDOL
PVSIIYHPQYTRQIGADIALLELEPXYKSSVHYVTYTPASETPRCMPQVDTG
GVDVNDLRPEPFKQVPIEMNHICDAKTHIGATYGGDVRIVRDMLCAGTRRD
SCQDSGSLPVCXVNGTWLQAGVVSMEGCAQPNRPGLYTRVYTLDMIHIVPKP"

ORIGIN
Alignment Scores:
Pred. No.: 1.16e-125 Length: 896
Score: 1405.00 Matches: 253
Percent Similarity: 94.91% Conservative: 8
Best Local Similarity: 92.00% Mismatches: 14
Query Match: 92.92% Indels: 0
DB: 9 Gaps: 0

US-09-598-982C-52 (1-275) x BC074974 (1-896)
Oy 1 MetLeuSerLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaAspPro 20
|||||.....

```

Db      34  ATGCTGAATCTGCTGCTGCTGGCGCTGCCCTTCGAGCCGCGCTTACGCGGCCCT 93
Qy      21  A|A|P|r|o|v|a|l|a|l|e|u|g|n|a|l|a|g|l|y|l|e|v|a|l|g|l|y|g|n|a|l|a|p|r|o|a|r|s|e| 40
Db      94  G|C|C|C|C|A|G|G|C|C|C|C|T|G|C|A|G|C|A|G|T|G|G|G|G|G|T|G|G|A|G|G|C|C|C|C|A|G|A|C| 153
Qy      41  l|y|s|e|r|p|r|o|t|p|g|l|n|a|l|e|u|g|n|a|l|a|g|l|y|l|e|v|a|l|g|l|y|g|n|a|l|a|p|r|o|a|r|s|e| 60
Db      154  A|A|G|T|G|C|C|C|T|G|C|A|G|C|A|G|T|G|G|G|G|G|T|G|G|A|G|G|C|C|C|C|A|G|A|C| 213
Qy      61  G|l|y|s|e|r|l|e|u|l|e|h|s|p|r|o|g|l|n|t|p|v|a|l|e|u|t|h|r|a|l|a|h|s|c|y|b|e|u|g|l|p|r|o|a|s|p|v|a|l| 80
Db      214  G|G|C|T|C|C|C|T|A|T|C|C|A|C|C|C|C|C|G|A|G|G|T|G|T|G|A|C|C|G|C|C|A|C|C|G|C|G|T|G|G|A|C|C|G|A|C|G|T|C| 273
Qy      81  l|y|s|a|s|p|l|e|u|a|l|a|t|h|r|e|u|a|r|g|v|a|l|g|n|l|e|u|a|r|g|l|n|h|s|l|e|u|y|t|y|t|p|m|e|h|i|s|p|h|e|c|y|s|g|l|y| 100
Db      274  A|N|G|A|T|C|T|G|G|C|C|C|C|T|C|A|G|G|G|G|G|C|A|A|C|T|G|C|G|G|A|C|A|C|C|T|T|A|C|T|A|C|C|A|G|A|C|C|A|G| 333
Qy      101  l|e|u|l|e|u|p|r|o|v|a|l|s|e|r|a|r|g|l|e|l|e|v|a|l|h|s|p|r|o|g|l|n|p|h|e|t|y|r|l|e|l|e|g|l|n|t|h|r|g|l|y|a|l|a| 120
Db      334  C|T|G|C|T|C|C|G|G|T|C|A|G|C|A|G|A|T|C|A|T|C|G|T|G|C|A|C|C|C|A|G|T|T|C|A|C|A|C|C|G|C|C|C|A|G|A|T|C|G|A|G|C|G| 393
Qy      121  A|s|p|l|a|l|e|u|e|u|g|l|u|e|u|g|l|u|p|r|o|v|a|l|a|n|h|l|e|s|e|r|s|e|r|a|r|g|v|a|l|h|s|t|h|r|v|a|l| 140
Db      394  G|A|C|A|T|G|C|C|C|T|G|G|A|G|C|T|G|G|A|G|C|C|G|G|T|G|A|G|G|T|C|C|A|G|C|C|A|G|C|C|A|G|C|C|A|C|G|G|T|C| 453
Qy      141  M|e|t|l|e|u|p|r|o|p|r|o|l|a|s|e|r|g|l|u|t|h|r|p|h|e|p|r|o|f|g|l|y|e|c|p|r|o|c|y|e|t|p|v|a|l|t|h|r|g|l|y|t|p| 160
Db      454  A|C|C|T|G|C|C|C|C|T|G|C|C|A|G|A|C|T|T|C|C|C|C|G|G|G|A|T|C|C|G|G|G|G|T|G|G|G|T|G|G|G|T|G|G|G|T|G|G|G|T|G|G| 513
Qy      161  G|l|y|a|s|p|v|a|l|a|s|p|h|a|s|p|l|u|p|r|o|l|e|u|p|r|o|p|r|o|p|h|e|p|r|o|l|e|u|s|g|l|n|a|l|l|y|s|v|a|l| 180
Db      514  G|G|G|A|T|G|G|A|C|A|T|A|T|A|T|A|G|C|C|C|T|C|C|C|A|C|C|G|C|C|A|T|T|C|T|C|T|G|A|A|G|A|G|G|G|A|A|G|G|T|C| 573
Qy      181  P|r|o|l|e|u|e|G|l|a|s|h|h|i|s|l|e|c|y|s|a|s|p|a|l|y|s|t|y|r|h|i|s|l|e|u|g|l|v|a|l|a|t|h|r|g|l|y|a|s|p| 200
Db      574  C|C|C|A|T|A|T|G|A|A|A|C|C|A|C|A|T|T|G|T|G|A|G|C|A|A|A|T|A|C|C|A|C|C|T|T|G|G|C|C|T|A|C|A|C|G|G|A|G|A|C| 633
Qy      201  A|s|p|v|a|l|a|r|g|l|e|l|e|a|r|g|a|s|p|h|e|l|e|u|c|y|s|a|l|a|g|l|y|a|s|n|s|e|r|g|l|n|a|r|g|a|s|e|r|c|y|s| 220
Db      634  G|A|C|G|T|C|C|G|C|A|T|G|C|G|T|G|A|C|A|C|A|T|G|T|G|G|G|G|A|A|C|A|C|C|G|G|A|G|G|A|G|C|T|A|T|G|C| 693
Qy      221  l|y|s|g|l|y|a|s|p|s|e|r|g|l|y|l|p|r|o|l|e|u|v|a|l|c|y|s|l|y|s|v|a|l|a|s|n|g|l|t|h|r|t|p|l|e|u|g|n|a|l|y| 240
Db      694  C|A|G|G|G|G|A|C|T|C|C|G|A|G|G|G|C|C|C|T|G|T|G|T|C|A|A|G|T|A|A|T|G|C|A|C|T|G|C|T|G|C|A|G|G|G|G|C| 753
Qy      241  v|a|l|v|a|l|s|e|r|t|p|a|s|p|g|l|u|g|l|c|y|s|a|l|a|g|l|n|p|r|o|a|s|a|r|g|p|r|o|g|l|y|l|e|t|y|r|h|a|r|g|v|a|l| 260
Db      754  G|T|G|T|A|G|C|T|G|G|G|C|A|G|G|G|C|T|G|T|G|C|C|A|G|C|C|C|A|C|C|G|G|C|T|G|G|C|A|T|C|T|A|C|A|C|C|G|T|G|T|C| 813
Qy      261  t|h|t|y|r|t|y|r|e|u|a|s|p|t|p|l|e|h|i|s|h|i|s|t|y|r|v|a|l|p|r|o|l|y|s|l|y|s|p|r|o| 275
Db      814  A|C|T|A|C|T|A|C|T|G|G|A|C|T|G|A|T|C|C|A|C|C|A|T|A|T|G|T|C|C|C|A|A|A|A|G|C|G| 858

```

```

FEATURES
source
    1..1143
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /map="16"
        /cell_type="mast cell"
        /tissue_type="lung"
        1..1143
        /gene="TPS2"
        /gene="TPS2"
        /product="beta-tryptase"
        6..833
        /gene="TPS2"
        /codon_start=1
        /product="beta-tryptase"
        /protein_id="AAA51843.1"
        /db_xref="GI:179584"
        /db_xref="DDB:G00-125-891"
        /translation="MLNLLALPYLASRAYAAPRGALRVGIVGGQEPKSKPM
QVSLKRVHPQYMMHFCGSLIHPQWLTAAHCVGDPVDKDLARVQLRQHLAYDQQL
EVSRIIVHPQYTAQIGADIALLELEPVKVSIVHTVTLPASBPSPGBCWVTGM
GDVNDERLPPFPKQVQVPMENHIIDAKYHSHGAYGDPVRIVRDMLCAGNTRD
SCQSGSGRLVKVKNVTLQAGVSVWSGSCAQPRPRGITYRVTVYLLDIHHYVPRKP"
        6..95
        /gene="TPS2"
        /note="G00-125-891"
        96..830
        /gene="TPS2"
        /product="beta-tryptase"
        /note="G00-125-891"

ORIGIN
Alignment Scores:
Pred. No.:      1,54e-125      Length:      1143
Score:          1405.00      Matches:      253
Percent Similarity: 94.91%      Conservative: 8
Best Local Similarity: 92.00%      Mismatches: 14
Query Match:      92.92%      Indels:      0
DB:              9      Gaps:      0

US-09-598-982C-52 (1-275) x HUMBTTRYP (1-1143)
Qy      1  MetLeuSerLeuLeuLeuLeuAlaleuProValleuAlaserArgAlaTyraAlaPro 20
Db      6  ATGCTGAATCTGCTGCTGCTGGCGCTGCCCTTCGAGCCGCGCTTACGCGGCCCT 65
Qy      21  A|A|P|r|o|v|a|l|a|l|e|u|g|n|a|l|a|g|l|y|l|e|v|a|l|g|l|y|g|n|a|l|a|p|r|o|a|r|s|e| 40
Db      66  G|C|C|C|C|A|G|G|C|C|C|C|T|G|C|A|G|C|A|G|T|G|G|G|G|G|T|G|G|A|G|G|C|C|C|C|A|G|A|C| 125
Qy      41  l|y|s|e|r|p|r|o|t|p|g|l|n|a|l|e|u|g|n|a|l|a|g|l|y|l|e|v|a|l|g|l|y|g|n|a|l|a|p|r|o|a|r|s|e| 60
Db      126  A|A|G|T|G|C|C|C|T|G|C|A|G|C|A|G|T|G|G|G|G|G|T|G|G|A|G|G|C|C|C|C|A|G|A|C| 185
Qy      61  G|l|y|s|e|r|l|e|u|l|e|h|s|p|r|o|g|l|n|t|p|v|a|l|e|u|t|h|r|a|l|a|h|s|c|y|b|e|u|g|l|p|r|o|a|s|p|v|a|l| 80
Db      186  G|G|C|T|C|C|T|A|T|C|C|A|C|C|C|C|G|A|G|G|T|G|T|G|A|C|C|G|C|C|A|C|C|G|C|G|T|G|G|A|C|C|G|A|C|G|T|C| 245
Qy      81  l|y|s|a|s|p|l|e|u|a|l|a|t|h|r|e|u|a|r|g|v|a|l|g|n|l|e|u|a|r|g|l|n|h|s|l|e|u|y|t|y|t|p|m|e|h|i|s|p|h|e|c|y|s|g|l|y| 100
Db      246  A|N|G|A|T|C|T|G|G|C|C|C|C|T|C|A|G|G|G|G|G|C|A|A|C|T|G|C|G|G|A|C|A|C|C|T|T|A|C|T|A|C|A|G|A|C|A|G| 305
Qy      101  l|e|u|l|e|u|p|r|o|v|a|l|s|e|r|a|r|g|l|e|l|e|v|a|l|h|s|p|r|o|g|l|n|p|h|e|t|y|r|l|e|l|e|g|l|n|t|h|r|g|l|y|a|l|a| 120
Db      306  C|T|G|C|T|C|C|G|G|T|C|A|G|C|A|G|A|T|A|T|A|T|A|G|C|C|C|A|C|C|A|G|T|T|C|T|A|C|A|C|C|G|C|C|A|G|A|T|G|G|A|G|C|G| 365
Qy      121  A|s|p|l|a|l|e|u|l|e|u|g|l|u|e|u|g|l|u|p|r|o|v|a|l|a|n|h|l|e|s|e|r|s|e|r|a|r|g|v|a|l|h|s|t|h|r|v|a|l| 140

```

LOCUS HUMBTTRYP 1143 bp mRNA linear PRI 31-OCT-1994
 DEFINITION Human beta-tryptase mRNA, complete cds.
 ACCESSION M37488
 VERSION M37488.1 GI:179583
 KEYWORDS beta-tryptase; mast cell serine protease; tryptase.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1143)
 MILLER,J.S., Moxley,G. and Schwartz,L.B.
 Cloning and characterization of a second complementary DNA for
 human tryptase
 JOURNAL U. Clin. Invest. 86 (3), 864-870 (1990)
 MEDLINE 90369005
 PUBMED 2203827

COMMENT Original source text: Human adult lung mast cell, cDNA to mRNA,

|||||
Db 366 GACATCGCCCTGCTGAGCTGAGAGACCGGTGAAGGTCTCCAGCAGCTCACCGCTC 425
|||
Qy 141 MetLeuProProAlaSerGluThrPheProGlyMetProCybTTPValThreGlyTTP 160
|||
Db 426 ACCGTGCCCCCTGCTCAGAGACCTTCCCCCGGGAGATGCCGTGTGGATCACTGCTGG 485
|||
Qy 161 GlyAspValAspAsnAspGluProLeuProProPheProLeuGlyGlnValLysVal 180
|||
Db 486 GCGGATGTGACAAATGATGAGCGCTCCACCGCATTTCTCTGAAACAGGTGAAGGTTC 545
|||
Qy 181 ProIleMetGluAsnHisIleCybAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
|||
Db 546 CCCATTAATGAAAACCACTTTGTATCCGAAATACCACTTGGCGCTTACAGCGAGAC 605
|||
Qy 201 AspValArgIleIleArgAspAspMetLeuCybAlaGlyAsnSerGlnArgAspSerCys 220
|||
Db 606 GACGTCCGCATGCTCGTGAAGCATGCTGTGTGCCGGGAAACACCGGAGGGACTCATGC 665
|||
Qy 221 LysGlyAspSerGlyGlyProLeuValCybLysValAsnGlyThrTTPLeuGlnAlaGly 240
|||
Db 666 CAGGCGCACTCCGGAGGGCCCTGTGTGTGCAAGGTGAATGGCACTGGCTGAGCGGGC 725
|||
Qy 241 ValValSerTTPAspGluGlyCybAlaGlnProAsnAspProGlyTyrTTPThrArgVal 260
|||
Db 726 GTGTGACCTGGGGCGAGGGCTGTGCTCCAGGCCCAACCGGCTGAGCATCTTACCCGTGTC 785
|||
Qy 261 ThrTyrTyrLeuAspTTPIleHisIleTyrValProLysLysPro 275
|||
Db 786 ACCCTACTGACTGGATGATGCACCATATGTCCCAAAAAGCCG 830
|||

RESULT 9

LOCUS S55551 1145 bp mRNA linear PRI 08-MAY-1993
DEFINITION beta-tryptase [human, basophil cell line KU812, mRNA, 1145 nt].
ACCESSION S55551
VERSION S55551.1 GI:265666
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1145)
AUTHORS Blom, T. and Hellman, L.
TITLE Characterization of a tryptase mRNA expressed in the human basophil cell line KU812
JOURNAL Scand. J. Immunol. 37 (2), 203-208 (1993)
MEDLINE 93166209
PUBMED 8434231
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI g1bbqg 125219] from the original journal article.
FEATURES
source
1..1145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..1145
/gene="beta-tryptase"
/note="precursor"
8..835
/gene="beta-tryptase"
/codon_start=1
/protein_id="AAD13876.1"
/db_xref="GI:4261576"
/translation="MLNLILALPYLASRAVAAPAGQALQRVGIVGQEARSKMP
QVSLRHGPYMMHFCGSLIHPOWVLTAAHCVGPVKDLAALRVGLRQDL
PVSRIIVHPOFTQIDIGADIALILEEYVAKSHHTVTLTPASSTPFGMP
GDVNDERLPPRPFLKQYKVRIMENHIDAKYHGLAYTGDDVRIYRDMLCANTRRD
SCQGSGBELVCVKNVGTWLDQGVSWBSCAOPNRPGLYTRVTYILDWTHIVPKP"

ORIGIN

Alignment Scores: 1.54e-125 length: 1145
Pred. No.:

Score: 1405.00 Matches: 253
Percent Similarity: 94.91% Conservative: 8
Best Local Similarity: 92.00% Mismatch: 14
Query Match: 92.92% Indels: 0
DB: 9 Gaps: 0

US-09-598-982c-52 (1-275) x S55551 (1-1145)

Qy 1 MetLeuSerLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaPro 20
|||
Db 8 ATGCTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
|||
Qy 21 AlaProValGlnAlaLeuGlnAlaGlyTyrLeuValGlyGlnGlnAlaProArgSer 40
|||
Db 68 CCCCCAGGCCAGGCCCTGCAAGCGAGTGGGCAATGCTTGGGGTCAAGAGCCCCCAGAGAC 127
|||
Qy 41 LysTTPProTTPGlnValSerLeuArgValArgAspArgTyrTTPMetHisPheCysGly 60
|||
Db 128 AAGTGGCCCTGGCAGGTGAGCTGAGATCCAGGCCCATCTGATGACATCTTCTGCGGG 187
|||
Qy 61 GlySerLeuIleHisPProGlnTTPValLeuThrAlaAlaHisCybLeuGlyProAspVal 80
|||
Db 188 GGTCTCCTCATCCACCCCAAGTGGGTCTGACCGCAGCGCACTGCGGAGCCGAGCGTC 247
|||
Qy 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGln 100
|||
Db 248 AAGATCTGGCGCCCTCAGGATGCACTGGGAGACAGACCTTCTTACAGAGACAG 307
|||
Qy 101 LeuLeuProValSerArgIleIleValHisPProGlnPheTyrIleIleGlnThrGlyAla 120
|||
Db 308 CTGCTGCGGTCAGACAGATCATGTCGACCAAGTTCATACACGCCAGATCGAGCG 367
|||
Qy 121 AspIleAlaLeuLeuGluLeuGluProValAsnIleSerSerArgValHisThrVal 140
|||
Db 368 GACATCCGCCCTGCTGAGCGAGTGAAGCTTCCACCGACAGTCCACAGCTC 427
|||
Qy 141 MetLeuProProAlaSerGluThrPheProProGlyMetProCybTTPValThreGlyTTP 160
|||
Db 428 ACCCTGCCCCCTGCTCAGAGACCTTCCCCCGGGAGATGCCGTCTGGGTCACTGGCTGG 487
|||
Qy 161 GlyAspValAspAsnAspGluProLeuProProPheProLeuGlyGlnValLysVal 180
|||
Db 488 GCGCATGTGACATGATGATGAGCGCTCCACCGCATTTCTCTGAAAGAGGTGAAGGTTC 547
|||
Qy 181 ProIleMetGluAsnHisIleCybAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
|||
Db 548 CCCATTAATGAAAACCACTTTGTGACGCAAAATACCACTTGGCGCTTACAGCGAGAC 607
|||
Qy 201 AspValArgIleIleArgAspAspMetLeuCybAlaGlyAsnSerGlnArgAspSerCys 220
|||
Db 608 GACGTCCGCATGCTCGTGAAGCATGCTGTGCTCCGGAACACCCGAGGAGACTCATGC 667
|||
Qy 221 LysGlyAspSerGlyGlyProLeuValCybLysValAsnGlyThrTTPLeuGlnAlaGly 240
|||
Db 668 CAGGCGCACTCCGAGGGCCCTGTGTGCAAGGTGAATGCACTGGCTGCAAGCGGGC 727
|||
Qy 241 ValValSerTTPAspGluGlyCybAlaGlnProAsnAspProGlyTyrTTPThrArgVal 260
|||
Db 728 GTGTGACCTGGGGCGAGGGCTGTGCCAGGCCAACCGGCTGCACTTACACCCGTGTC 787
|||
Qy 261 ThrTyrTyrLeuAspTTPIleHisIleTyrValProLysLysPro 275
|||
Db 788 ACCCTACTGACTGGATGATGCACCATATGTCCCAAAAAGCCG 832
|||

RESULT 10
LOCUS BC029356 1194 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens tryptase beta 2, mRNA (cDNA clone MGC:32523
IMAGE:4695458), complete cds.
ACCESSION BC029356
VERSION BC029356.1 GI:20809954
KEYWORDS MGC.
SOURCE Homo sapiens (human)

	ORGANISM
	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1194)
REFERENCE	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschuler,S.F., Zeeberg,B., Blotow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F., Diatchenko,L., Marinsin,K., Farmer,A.A., Rubin,G.W., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scieczek,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abrahamson,R.D., Mulihay,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.U., Malek,J.A., Gunaratne,P.H., Richards,S., Wotley,K.C., Hale,S., Garcia,A.M., Gay,L.U., Hultk,S.W., Villalton,D.K., Muzny,D.M., Sodergren,E.-J., Lu,X., Gibbs,R.A., Fahey,J.J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butcherfield,Y.S., Krzywinski,M.I., Skalska,U.V., Smalls,D.E., Schnierfeld,A., Schein,J.E., Jones,S.J. and Marx,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
JOURNAL	2 (bases 1 to 1194)
PUBLISHED	Strausberg,R.
REFERENCE	Direct Submission
AUTHORS	Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
JOURNAL	NIH-MGC Project URL: http://mgc.nci.nih.gov
REMARK	Contact: MGC help desk
COMMENT	Email: gcgaps-remail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.sngc.stanford.edu Contact: (Dickson,Mark) mcdexpaill@stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.nyu.edu Series: IRAL Plate: 41 Row: j Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13775596. Location/Qualifiers 1..1194 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:32523 IMAGE:4635458" /tissue_type="Lung" /clone_lib="NIH MGC_77" /lab_host="DH10B" /note="Vector: pDNR-LIB" 1..1194 /gene="TPSB2" /db_xref="locusID:64499" 24..851 /gene="TPSB2" /codon_start=1 /product="tryptase beta 2, precursor" /protein_id="AAH29356.1" /db_xref="GI:20809955" /db_xref="LOCUSID:64499" /translation="MTNLTLLATLVLASRAYAAPGQALRVGVISGGAEPRSKRW OVSRIVGVPIWMHF CGSLIHPVLIPQAVLPAHCVGPDVDIALRVQLREGHLYYODPLL
CDS	

ALIGNMENT SCORES:			
Alignment Scores:	1.62e-125	Length:	1194
Pred. No.:	1405.00	Matches:	253
Score:	94.91%	Conservative:	8
Best Local Similarity:	92.00%	Mismatches:	14
Query Match:	92.92%	Indels:	0
DB:	9	Gaps:	0
US-09-598-982C-52 (1-275) x BC029356 (1-1194)			
QY	1 MetLeuSerLeuLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTYrAlaAlaPro	20	
DB	24 ATGCTGATCTGCTGCTGCTGCGCTGCCGCTCCGTCGAGCGCGCTACGGCGCCCTC	83	
QY	21 AlaProValGlnAlaLeuGlnGlnAlaGlyTLeValGlyGlyGlnGlnAlaProArgSer	40	
DB	84 GCCCCAGGCCAGGGCCCTGCAGCGAGTGGGATGTTGGGGGTGAGAGGGCCCCAGGAGC	143	
QY	41 LysTrpProTrpGlnValSerLeuArgValArgAspArgTYrTrpMetHispeCysGly	60	
DB	144 AAGTGGCCCTGGCGAGTGAAGCCTGAGAGTCCAGGCCCATCTGGATGCATCTTGGGG	203	
QY	61 GlySerLeuLeuHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal	80	
DB	204 GGCTCCCTCATCCACCCCGAGTGGGTCTGACCGCAGCGCATGCGGGAGACCGGACGTC	263	
QY	81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlyGlnHisLeuTYrTYrGlnAspGln	100	
DB	264 AAGGATCTGGCGCGCCCTCAGAGGTGCACCTCGGGAGAGAGACCTCTACCTACAGAGCAG	323	
QY	101 LeuLeuProValSerArgLeileValHisProGlnPheTYrTLeileGlnThrGlyAla	120	
DB	324 CTGCTGCCGCTCAGCAGATCATCTGCACCCACAGTTCTTACACCGCCAGATCGGAGCG	383	
QY	121 AspIleAlaLeuLeuGlnLeuGlnGluProValAsnIleSerSerArgValHisThrVal	140	
DB	384 GACATGCCCTCGCTGAGCGTGGAGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTC	443	
QY	141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThrGlyTrp	160	
DB	444 ACCCTGCCCTGCTCTCAGAGACCTTCCCCCGGGAGTGCCTGTGCTGGTCACTGGCTGG	503	
QY	161 GlyAspValAspAsnAspGluProLeuProProProPheProLeuLysGlnValLysVal	180	
DB	504 GGCATGTGGCAATGATGAGCGCCTCCACCGCATTTCTCTGAAGCAGGTGAAGTTC	563	
QY	181 ProIleMetGluAsnHisIleCysAspAlaLysTYrHisLeuGlyAlaTYrThrGlyAsp	200	
DB	564 CCCATATGAGAAACCACTTTGTGAGCGCAAAATACCACTTGGCGCTTACCGGAGAC	623	
QY	201 AspValArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys	220	
DB	624 GACCTCGGCATCGCCGCTGACGACATCTGTGTGCCGGGAACACCCGAGGGACTCATGC	683	
QY	221 LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGly	240	
DB	684 CAGGCGCACTCCGAGGGGCCCTGGTGTGGAAGGTGAATGACACTGGCTGCAGGGCGGC	743	
QY	241 ValValSerTrpAspArgGlyGlyCysAlaGlnProAsnArgProGlyIleTYrThrArgVal	260	
DB	744 GTGTCTAGCTGGGGCGAGGCTGTGGCCAGCCACCGGCTGGCATCTACCCCGTGTCTC	803	
QY	261 ThrTYrTYrLeuAspTrpIleHisHisLeTYrValProLysLysPro	275	
DB	804 ACCTACTACTTGACTGGATCCACCACTATGTCTCCCAAAAGCGG	848	

LOCUS	BC038416	1235 bp	mRNA	linear	PRI 25-JUN-2004
DEFINITION	Homo sapiens tryptase beta 2, mRNA (CDNA clone IMAGE:5176645), partial cds.				
ACCESSION	BC038416				
VERSION	BC038416.1	GI:23512304			
KEYWORDS	.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				

SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 1460)
AUTHORS	Strausberg,R.L., Collins,F.S., Wagner,L.H., Derge,J.H., Klausner,R.D., Collins,F.S., Wagner,L.H., Shennan,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T.I., Max,S.I., Wang,J., Heien,F., Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Udell,T.B., Toshiyuki,S., Grancini,P., Prange,C., Raha,S.S., Loguanello,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosk,S.A., McEwan,P.J., McCreann,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Woley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Young,A.C., Shcherbenko,Y., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shcherbenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Girmwood,J., Schmutz,J., Myers,R.M., Buttefield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2 (bases 1 to 1460)
AUTHORS	Director MGC Project.
TITLE	Direct Submission
JOURNAL	Submitted (02-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov Akter,N., Ayele,K., Beckertson-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooke,S., Dietrich,N.L., Grante,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,F., Legaapi,R., Maduro,Q.L., Mastello,C., Maheux,B., Mastlin,S.D., McCloskey,J.C., McComell,J., Pearson,R., Stantirou,S., Thomas,P.J., Touchman,J.W., Tsurugson,C., Vogt,J.L., Walker,M.A., Weherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov Series: IRAX Plate: 139 Row: n Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gl: 13775596.
SOURCE	Location/Qualifiers 1..1460 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:74871 IMAGE:5752632" /tissue_type="Brain, Lung, Testis, adult, pooled whole" /clone_id="NIH_MGC_115" /lab_host="DH10B" /note="vector: pCMV-SPORT6" 1..1460 /gene="PPSPB2" /db_xref="LocusID:64499" 191..1039

		/gene="TPSB2"	
		/codon_start=1	
		/product="TPSB2 protein"	
		/protein_id="AAH65923.1"	
		/db_xref="GI:41944665"	
		/db_xref="LOCUSID:64499"	
		/translation="MLLAPQMLNLALLPVLASRAYAAPAQALORVGI VGGQ PRKAMQVSLRVHPHYMMFGGSLIHPOVLTIAHVGVDDILALRQLRE YYDQLLPVSRILIVHPPTIATGDIDLILLEPVKSSHHVTYIPASEFP PCWTVTMSDVNDERLPPFPLKVQVTKIMENHICDAKYHLGAITGDVRI VRDDMI AGNTRDSRCQSGSGLPVCKNVGTWLQAGVVSWGEGCAQPNRPAI YTRITYYLDWI YVPKKP"	
ORIGIN			
Alignment Scores:	2.05e-125	Length: 1460	
Pred. No.: 1405.00	Matches: 253		
Score: 94.91%	Conservative: 8		
Percent Similarity: 92.00%	Mismatches: 14		
Best Local Similarity: 92.92%	Indels: 0		
Query Match: 9	Gaps: 0		
DB:			
US-09-598-982C-52 (1-275) x BC065923 (1-1460)			
Oy	1 MetLeuSerleuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaAlaPro	20	
Db	212 ATGCTAATTCGTGCTGCTGGCGCTGCCCGCTGGGAGCGCGCTACGCAGCCCT	271	
Oy	21 AlaProvalGlnAlaLeuGlnGlnAlaGlyLevalGlyGlnGlnAlaProArgSer	40	
Db	272 GCCCAAGCCAGGCCCTCGACGCAAGTGCGCATCTGGGGGTCAGAGAGCCCCAGAGAGC	333	
Oy	41 LysTrpProTrpGlnAlaSerleuArgValArgAsparGlyTrpMetHisPheCysGly	60	
Db	332 AAGTGCGCCCTGGCAGGTGAGCTGAGAGTCCAGCCCATCTGGATCATCTTCGCGGG	391	
Oy	61 GlySerleuLeuHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal	80	
Db	392 GGCCTCCCTCATCCACCCTCAGTGGGTCTGACCGCAGCGCATCTGTTGGAGCCGAGCGTC	451	
Oy	81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGln	100	
Db	452 AAGGATCTGGCCGCCCTCGAGGTCGACACTGCCGAGCAGACACTTAACAAGAAGCAG	511	
Oy	101 LeuLeuProValSerArgLeilelleValHisProGlnPheTyrLeileGlnThrGlyAla	120	
Db	512 CTGCTGCGGTCAGCAGATCATCTCGGCACCCAGACTTCTACACCGCCAGATCGAGAGCG	571	
Oy	121 AspTlleAlaLeuLeuGlnLeuGlnGluProValAlaenIlleSerSerArgValHisThrVal	141	
Db	572 GACATGCGCTCTGTCGAGCTTGAGGAGCGCGGTGAAGGTCCTCCAGCACAGTCCACACGCTC	631	
Oy	141 MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTrpValThnGlyTyr	160	
Db	632 ACCCTGCCCCCTCCTCAAGACCTTCCCCCGGGGAATGCCGTGCTGGTACTACGTGGCTGG	691	
Oy	161 GlyAspValAspAsnAspGluProLeuProProPheProLeuLysGlnValLysVal	180	
Db	692 GGGAATGTGACAAATATAGAGGCGCTCCACCGCATTTCTCTGAAGCAGAGTGAAGGTC	751	
Oy	181 ProIleMetGlnAsnHisIleCysAspAlaLysTyrHisLeuGlnAlaTyrThrGlyAsp	200	
Db	752 CCCATATATGAAAAACACACATTGTCAGCAAAATACCACTTGGGCGCTTACACGGAGAAC	811	
Oy	201 AspValArgIleLeuArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys	220	
Db	812 GACGTCCGATCTCTCTGACGACATGCTGTCTCGGGAAACACCCGGAGGAGACTCATGC	871	
Oy	221 LysGlyAspSerGlyGlyProLeuValCysLysValLaangIYThrTrpLeuGlnAlaGly	240	
Db	872 CAGGCGCATCTCCGAGAGGCGCTCTGGTGTGCAAGTGAATGACACTGCTGACAGCGGCGC	931	
Oy	241 ValValSerTrpAspGlnGlyCysAlaGlnProAsnArgProGlyLleTyrThrArgVal	260	

Db 721 GTGCTAGCTGGGGCGAGGCGCTGTGCCCGACGCCAGCGGCTGGCATCTACACCGGTTC 780
Qy 261 ThrTyrTyrLeuAspTrrPleHisHisTyrValProLysLysPro 275
Db 781 ACTTACTTGTGACTGATCCACCACTATGTCTCCCAAAAAGCCG 825
RESULT 14
AR080460 AR080460 1137 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 13 from patent US 5968782.
DEFINITION AR080460
ACCESSION AR080460
VERSION AR080460.1 GI:10007195
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1137)
AUTHORS Stevens, R.L.
TITLE Mast cell protease that cleaves fibrinogen
JOURNAL Patent: US 5968782-A 13 19-OCT-1999;
FEATURES
source location/Qualifiers
1. 1137
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 2.98e-125 Length: 1137
Score: 1402.00 Matches: 252
Percent Similarity: 95.24% Conservative: 8
Best Local Similarity: 92.31% Mismatches: 13
Query Match: 92.72% Indels: 0
DB: Gaps: 0
US-09-598-982C-52 (1-275) x AR080460 (1-1137)
Qy 3 SerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaProAlaPro 22
Db 3 AATCTGCTGCTGCTGCGCTGCCGCTCTGCGCAGCGCGCTTACCGCGCCCTGCCCA 62
Qy 23 ValGlnAlaLeuGlnGlnAlaGlyTyrValGlyGlnGlnAlaProArgSerLysTrp 42
Db 63 GGCAGGCGCTGCGAGGAGTGGGCGATGTCGGGGTCAAGAGGCGCCCGAGAGCAAGTGG 122
Qy 43 ProTrGlnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGlyLysSer 62
Db 123 CCTGGCAGGTGAGCTGAGAGTCCAGGCCATCTGATGTGACTTCTGGCGGGCTCC 182
Qy 63 LeuIleHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspValLysAsp 82
Db 183 CTCATCCACCCCGACAGTGGGTGCTGACCGCAGCTGCTGGGACCGGACGTCAGAGAT 242
Qy 83 LeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGlnLeu 102
Db 243 CTGGCGCGCTCGAGGTGCACTGCGGAGCAGCACTTACTTACAGAGCAAGCTGCTCG 302
Qy 103 ProValSerArgLleIleValHisProGlnPheTyrLleIleGlnThrGlyAlaAspIle 122
Db 303 CCGGTGAGCAGATCATCGTGCACCCACAGTTCTTACACCGCCAGATCGGAGGAGCATC 362
Qy 123 AlaLeuLeuGlnLeuGlnLupProValAsnLleSerSerArgValHisThrValMetLeu 142
Db 363 GCGCTCTGGAGCTGAGGAGCGCGGTGAACGTCTCCAGCCACCTCCACAGCGTCAACCCG 422
Qy 143 ProProAlaSerGlnThrPheProProGlyMetProCysTyrValThrGlyTrrGlyAsp 162
Db 423 CCCCCTGCTCAAGACCTTCCCCCGGGGATCCGTGCTGGTCACTGGCTGGGGCGAT 482
Qy 163 ValAspAsnAspGlnProLeuProProProProPheProLeuLysGlnValLysValProIle 182
Db 483 GTGAGACATGATAGGGCGTCCACCGCATTTCTCTGAAGCAGGTGAAGTCCCCCA 542
Qy 183 MetGlnAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspVal 202

Db 543 ATGAAAAACCAATTGTGAGCGCAAAATACCACTTGGCGGCTTACAGCGGAGACGATC 602
Qy 203 ArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCysLysGly 222
Db 603 CGCATCTGCTCGTGAAGCATGTCTGTCTCCGGGAACACCCGAGAGGATCTATGCCAGGGC 662
Qy 223 AspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValVal 242
Db 663 GACTCCGGAGGGCGCCCTGGTGTGCAAGGTGAATGGACCTGGCTGCAGCGCGCGTGGTTC 722
Qy 243 SerTrpAspGlnGlyCysAlaGlnProAsnArgProGlyTyrIleTyrThrArgValThrTyr 262
Db 723 AGCTGGGCGAGGCGTGTGTGCCAGCCCAACCGGCTGGCATCTTACACCGGTGTCACTAC 782
Qy 263 TyrLeuAspTrrPleHisHisTyrValProLysLysPro 275
Db 783 TACTTGGACTGATTCACCATATGTCTCCCAAAAAGCCG 821

RESULT 15
HUMTRYIA 1137 bp mRNA linear PRI 03-AUG-1993
LOCUS Human tryptase-I mRNA, 3' end.
DEFINITION M33491
ACCESSION M33491.1 GI:339980
VERSION M33491.1 GI:339980
KEYWORDS serine protease; tryptase-I.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1137)
AUTHORS VanderSlie, P., Ballinger, S.M., Tam, E.K., Goldstein, S.M.,
Craik, C.S. and Caughey, G.H.
TITLE Human mast cell tryptase: multiple cDNAs and genes reveal a
multigene serine protease family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (10), 3811-3815 (1990)
MEDLINE 90251647
PUBMED 2187193
COMMENT Original source text: Human adult skin, cDNA to mRNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by P.Vanderslie, 02-APR-1990.
FEATURES
source location/Qualifiers
1. 1137
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
<1..824
/note="tryptase-I"
/codon_start=3
/protein_id="AAA36778.1"
/db_xref="GI:339981"
/translation="MLILALPVLASRAYAAPARQALQRVGIVGGGEAPRSKMPQV
SLRVGPFWMHRCGSLHLPQWVLTAAICVDPVYDLALAESEIPEQHLVYQDQLLPV
SRIVHPQVTAIOIGADILALLEBPVVSHTVTLPPASEIPEPCMPGVGMGD
VDNDRLPPLPPKQVYKPIEMNHICDKKHLGATGDAIVYDDMLCAINTPRDSC
QGDSGLPVLCVKNVTLDAGVSWEGCAQPNRPETIYRVITYVIMIHIVPKRP"
1119..1124

ORIGIN
polyA_signal
Alignment Scores:
Pred. No.: 2.98e-125 Length: 1137
Score: 1402.00 Matches: 252
Percent Similarity: 95.24% Conservative: 8
Best Local Similarity: 92.31% Mismatches: 13
Query Match: 92.72% Indels: 0
DB: Gaps: 0
US-09-598-982C-52 (1-275) x HUMTRYIA (1-1137)

Qy 3 SerLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaProAlaPro 22
Db 3 AATCTGCTGCTGCTGCGCTGCCGCTCTGCGCAGCGCGCTTACCGCGCCCTGCCCA 62

This page Blank (just to)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2005, 15:00:06 ; Search time 3116 Seconds
(without alignments)
3359.331 Million cell updates/sec

Title: US-09-598-982C-52

Perfect score: 1512
Sequence: 1 MSLILLALPVLASRAVAP.....ITRTVTVLDVIMHVKKP 275

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2.1/USPTO.apool.p/US0598982/crunat.29082005.080946.26105/app_query.fasta_1.455
-DB=EST -QFMT=fasta -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human0.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0598982@cgn2.1.5180@crunat.29082005.080946.26105 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEBUFFER -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1463	96.8	1030	5	BM919268 AGENCOURT
2	1204.5	79.7	904	5	BM720404 AGENCOURT
3	1129	74.7	619	6	CD671851 fg07g11.y
4	1119	74.0	631	7	CV030374
5	1116.5	73.8	673	6	CD616760
6	1098.5	72.7	682	6	CD616759
7	1081	71.5	642	6	CD672689
8	1057.5	69.9	806	7	CF553058
9	1044	69.0	930	6	CB203717

10	1039	68.7	635	6	CD671891	CD671891 fg08b10.y
11	1029	68.1	1000	4	BT143250	BT143250 602986390
12	1006	65.5	589	5	BU071733	BU071733 im33a09.y
13	989.5	66.4	811	4	BG697540	BG697540 602660760
14	959	63.4	581	5	BU787772	BU787772 1034c08.y
15	923	61.0	736	4	BG542089	BG542089 602503309
16	905	59.9	678	4	BG483591	BG483591 602503309
17	900	59.5	647	6	CD631944	CD631944 56015309J
18	897	59.3	722	5	BK091892	BK091892 BX091892
19	891	58.9	512	2	BF724180	BF724180 bx01h02.y
20	866	57.3	502	5	BQ082929	BQ082929 K-EST0144
21	846	56.0	859	7	CF583025	CF583025 AGENCOURT
22	830	54.9	671	6	CB840425	CB840425 M1SE-0715
23	823	54.4	929	7	CF583026	CF583026 AGENCOURT
24	818	54.1	639	1	AA131142	AA131142 t213b01.t
25	808.5	53.5	553	6	CD631946	CD631946 56015325J
26	807	53.4	674	7	CK967791	CK967791 4083412.B
27	796	52.6	917	5	BQ721078	BQ721078 AGENCOURT
28	767	50.7	686	5	BU073263	BU073263 im33a09.x
29	742	49.1	558	4	BT790801	BT790801 id09c06.y
30	714	47.2	719	5	BK922783	BK922783 BX922783
31	705	46.6	731	7	CK770530	CK770530 958715.MA
32	697	46.1	1219	3	AK081986	AK081986 Mus_muscu
33	693	45.8	474	2	AW823937	AW823937 uf61e03.y
34	691	45.7	391	1	AJ714198	AJ714198 AJ714198
35	690.5	45.7	676	4	BG964077	BG964077 602828831
36	677	44.8	371	2	BF359130	BF359130 QV3-ET006
37	675	44.6	620	1	AA049080	AA049080 mj50F09.t
38	667	44.1	688	5	BQ003361	BQ003361 UI-H-E11-
39	662	43.8	693	5	BM991728	BM991728 UI-H-DP1-
40	659	43.6	527	6	CD631943	CD631943 56015309H
41	657	43.5	699	6	CA438721	CA438721 UI-H-DT1-
42	655	43.3	525	4	BT775716	BT775716 468400.MA
43	654	43.3	541	4	BA167216	BA167216 460544.MA
44	654	43.3	581	6	CA867421	CA867421 1r28f02.y
45	651	43.1	433	7	CK826343	CK826343 1034c08.y

ALIGNMENTS

RESULT 1
BM919268
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1030)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: <http://image.llnl.gov>
High quality sequence at: 719.
FEATURES
source
1..1030
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5748499"

/lab_host="DH10B"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 constructed and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH-MGC library."

ORIGIN

Alignment Scores:
 Pred. No.: 7,64e-133 Length: 1030
 Score: 1463.00 Matches: 270
 Percent Similarity: 98.92% Conservative: 4
 Best Local Similarity: 97.47% Mismatches: 1
 Query Match: 96.76% Indels: 2
 DB: Gaps: 0

US-09-598-982C-52 (1-275) x BW919268 (1-1030)

QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaPro 20
 DB 33 ATGCTAGAGCTGTGCTGTGGCTGCGCTCTGCGAGCCCGCTTACGCGGCCCT 92
 QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyLeValGlyGlnGlnAlaProArgSer 40
 DB 93 GCCCGGCTCAGGCGCTTGCAGCAGCGGGATGCTGGGGGTCAAGAGGCCCGGAGACC 152
 QY 41 LysTrpProTrpGlnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGly 60
 DB 153 AAGTGGCCCTGGAGGAGTGAAGCTGAGAGTCCGCGACCGATCGATGACATTCGTGGG 212
 QY 61 GlySerLeuLeuLeuHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
 DB 213 GGCTCCCTATCCACCCCGAGTGGTGTGACCGCGCGCAGCTTGGAGCCGAGCGTC 272
 QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTrpGlnAspGln 100
 DB 273 AAGGATCTGGCCACCTTCAGGGTGGCACTGGGAGACAGACCTTACTACAGAGACCG 332
 QY 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120
 DB 333 CGCTCCCGGTGAGCAGATCATCTGCACCCACATTCATCATCTCCAGACTGGAGCG 392
 QY 121 AspIleAlaLeuLeuGlnLeuGlnGlnProValAsnIleSerSerArgValHisTrpVal 140
 DB 393 GATATCGCCCTGTGAGCTGGAGGAGCGCGTGAACATCTCCAGCGCGCTCCACACGGTC 452
 QY 141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThrGlyTyr 160
 DB 453 ATGCTGCCCTGCTCGAGAGACTTCCCCCGGGAGATGCGTGGTGTCACTGGCTGG 512
 QY 161 GlyAspValAspAsnAspGluProLeuProProProPheProLeuLysGlnValLysVal 180
 DB 513 GCGCATGTGAGACATATGATGAGCCCTCCACCGCCATTTCCCTGAAGAGAGGAAAGTTC 572
 QY 181 ProIleMetGluAsnHisIleCysAspAlaLysTyrHisIleGlnAlaLysTyrThrGlyAsp 200
 DB 573 CCGATATGCAAAACCACTTGTGACGCAAAATATCACCTTGGCCCTTACACGGGAGAC 632
 QY 201 AspValArgIleIleArgAspAspMetLeuCysAlaGlyAsnSerGlnArgAspSerCys 220
 DB 633 GAGCTCCGATCATCTCGTGAACACATGCTGTGTGGGAGAACCCCGGAGGAGCTCATCT 692
 QY 221 LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGly 240
 DB 693 CAGGGGAGACTCTGGAGGCGCCCTGTGTGCAAGGTGAATGGACCTGGGTACAGGGGGC 752
 QY 241 ValValSerTrpAspGluGlyCysAlaGlnProAsnArgProGlyIleTyrTrpArgVal 260

DB 753 GTGTCAAGCTGGGAGCAGAGGGCTGTGCCACGCCCGGCTGGCATCTACACCCGTG 812
 QY 260 aAThTyrTrpLeuAspTrpIleHisIleTyrValProLysIleAspPro 275
 DB 813 TCACTTACTTGTGACTGGATTCACACTATGTATGCTCCCAAAAGCCG 859

RESULT 2
 BQ720404
 LOCUS
 DEFINITION
 AGENCOURT 8477973 lupski_sympathetic_trunk Homo sapiens cDNA clone
 IMAGE:6196776 5', mRNA sequence.
 ACCESSION
 BQ720404
 VERSION
 BQ720404.1 GI:21859301
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 1 (bases 1 to 904)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: LNL13605 row: m column: 01
 High quality sequence stop: 587.

FEATURES

source

1..904
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6196776"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski sympathetic trunk"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming.
 directionally cloned using the following adaptors:
 5'-TCGACCAAGGCTCCG-3' and
 5'-GACTAGTCTAGATCGAGCGGCCGCTT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."

ORIGIN

Alignment Scores:
 Pred. No.: 1.5e-107 Length: 904
 Score: 1204.50 Matches: 225
 Percent Similarity: 88.06% Conservative: 11
 Best Local Similarity: 83.96% Mismatches: 21
 Query Match: 79.66% Indels: 11
 DB: Gaps: 1

US-09-598-982C-52 (1-275) x BQ720404 (1-904)

QY 1 MetLeuSerLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaPro 20
 DB 10 ATGCTAGATCTGTCTGTGCGCTGCGCTCTGCGAGCCCGGCTTACGCGGCCCT 69
 QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyLeValGlyGlnGlnAlaProArgSer 40
 DB 70 GCCCGGCTCAGGCGCTTGCAGCAGTGGCATCTGTGGGGGTCAAGAGGCCCGGAGAGC 129

QY 41 LysTrpProTglnValSerLeuArgValArgAspArgTyrTrpMetHispeCysGly 60
DB 130 AAGTGGCCCTGGACAGTACGCTGAGATCCCGACCCGACTGATGATGATCTTCTGGG 189
QY 61 GlySerLeuLeuHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
DB 190 GGCTCCCTCATCCACCCCGAGTGGGTGACCGGACCGCACTGCTGGGACCG----- 243
QY 81 LysAspLeuAlaThrLeuArgValGlnLeuAagGlnGlnHisLeuTyrTyrGlnAspGln 100
DB 244 -----GTGCACTCGCCGAGCGACACTTACTACTACGAGACAG 282
QY 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleGlnThrGlyAla 120
DB 283 CTGCTCCCGGTGACAGATCATCTGTGACCCACGATTTCTTACACCGCCCAAGTGGAGCG 342
QY 121 AspIleAlaLeuLeuGlnLeuGlnGluProValAsnIleSerSerArgValHisThrVal 140
DB 343 GACATCGCCCTGTGAGCTGAGGAGCGCGGTGAACGTCTCCAGCCAGCTCCACCGGTC 402
QY 141 MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTyrValThrGlyTrp 160
DB 403 ACCCTGCCCCCTGCTCAGAGACCTTCCCGCGGAGATGCGCTGCTGGGTCACTGCTGG 462
QY 161 GlysAspValAspAsnAspGluProLeuProProProPheProLeuLeuGlnValLysVal 180
DB 463 GCGGATGGAGCAATGATGAGCGCTCCACCGCAATTTCTTAAAGAGAGGTGAAGGTC 522
QY 181 ProIleMetGluAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
DB 523 CCCATATATGAAACACACTTTGTGACGCAAAATCCACTTGGGCGCTACACGCGGAGAC 582
QY 201 AspValAlaGlieIleIleArgAspAspMetLeuCysAlaGlnProAsnArgProGlyIleTyrThr 220
DB 583 GACGTCCCGATGCTCGTGACACATGCTGTGTGCGGAGAACCCCGGAGGACATCATGC 642
QY 221 LysGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrThrLeuGlnIleGly 240
DB 643 CAGGGCGACTCCGAGAGGCGCTGTTGGGCAACGCGAATGCGCCCTGGGTGACACGGGC 702
QY 241 Val-ValSerTrpAspGluGlyCysAlaGlnProAsnArgProGlyIleTyrThr-ArgV 260
DB 703 GTGGGTCACTGGGCGGAGGCTGGGCGCCGCGCAACGCGGCGGCTTCTACACCCCGGG 762
QY 260 alThrTyrTyrLeuAspTrp 266
DB 763 CCGCGTCTACTGGAATGG 782

RESULT 3
CD671851
LOCUS CD671851 619 bp mRNA linear EST 24-JUN-2003
DEFINITION fg07g11.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
CD671851 5', mRNA sequence.
ACCESSION CD671851.1 GI:32173582
VERSION CD671851.1 GI:32173582
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 619)
Wistow, G., Bernslein, S.L., Ray, S., Wyatt, M.K., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
Mol. Vis. 8 (4), 185-195 (2002)
JOURNAL MEDLINE 22103462
PUBMED 12107412
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 07 row: 9 column: 11
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..619
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fg07g11"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH108"
/clone_lib="Human Iris cDNA (Normalized): fg"
/note="Organ: Eye; Vector: pCMVSPORT; A human iris library (bx) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (COT 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN
Alignment Scores:
Pred. No.: 2.27e-100 Length: 619
Score: 1129.00 Matches: 202
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 98.54% Mismatches: 0
Query Match: 74.67% Indels: 0
DB: Gaps: 0

US-09-598-982C-52 (1-275) x CD671851 (1-619)
QY 34 GlyGlnGluAlaProAspSerLeuTyrProTglnValSerLeuArgValArgAspArg 53
DB 3 GGTACGAGAGGCCCCACGAGACAGTGGCCCTGGCAGAGGACCTGAGAGTCCGGACCGCA 62
QY 54 TyrTrpMetHispeCysGlyGlySerLeuLeuHisProGlnTrpValLeuThrAlaAla 73
DB 63 TACTGATGACACTTCTGTGGGGGCTCCCTCATCCACCCCGAGTGGTGTGACCGCGCG 122
QY 74 HisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValGlnLeuAagGlnGln 93
DB 123 CACTGCCCGGAGCCGAGCTGACAGATCTGGCACTCCAGAGGTGCAACTCGGAGAGAG 182
QY 94 HisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHisProGlnPhe 113
DB 183 CACTCTTCTTCCAGAGACACTGCTGCGGTCAAGATCATCTGTCAACCACTTC 242
QY 114 TyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnLeuGlnGluProValAsnIle 133
DB 243 TACATCATCCAGATCGAGCGGATATGCGCTGTGAGCTGAGAGACCGGTGAACATC 302
QY 134 SerSerArgValHisThrValMetLeuProProAlaSerGluThrPheProProGlyMet 153
DB 303 TCAGCCCGCGTCCACACGCTATCTGCCCCCTCGGAGACCTTCCCGCGGAGTG 362
QY 154 ProCysTrpValThrGlyTyrGlyAspValAspAsnAspGluProLeuProProPhe 173
DB 363 CCGTCTGGGTCACTGCTGGGCGGATGTGACATATAGACCCCTCCACCGCCCATTT 422
QY 174 ProLeuGlnValLysValProIleMetGluAsnHisIleCysAspAlaLysTyrHis 193
DB 423 CCGTGAGAGCAGTGAAGTCCCATATAGAAAACACATTTGTGACGCAAAATACAC 482

QY	194	Leu51y1a1aYrrTrnG1yAaspApy1a1rG1le1le1a2yAaPaSPMeLeUcYal1aG1Y	213
Db	483	CTTGCGCGCTACACGGAGACGACGCTCCGACATCATCCGTGACGACATCTGTGTCCGGG	542
QY	214	AsnSerg1naYaspSerYcYalysG1yAaspSerg1yG1yProLeuValCys1yVala1sn	233
Db	543	AACACCGGAGGAGCTCATGCGCAGGCGACCTGTGAGGGCCCTGTGTGCAAGGTGAAT	602
QY	234	G1yThrTrpLeuGln	238
Db	603	GGCAGCTGGCTACAG	617
RESULT 4			
CV030374			
LOCUS			
DEFINITION	9476 Full length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC028059, mRNA sequence.		
ACCESSION	CV030374		
VERSION	CV030374.1	GI:51488624	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 631)		
AUTHORS	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Clingingsmith,T.R., Hartley,J.L., Eposito,D., Cheo,D., Moore,T., Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C., Vandenhaute,J., Cusick,M.E., Albaladejo,J.S., Hill,D.E. and Vidal,M. Human ORFome Version 1.1: a platform for Reverse Proteomics Genome Res. (2004) In press		
TITLE	Contact: Vidal M		
JOURNAL	Marc Vidal laboratory		
COMMENT	Dana Farber Cancer Institute 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA Tel: 617 632 5180 Fax: 617 632 5739 Email: Marc.Vidal@dfci.harvard.edu ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers PCR Primers FORWARD: ATGCTGAGCCTGCTGCTG BACKWARD: CACGGCTTTTGGGACATA Insert Length: 631 Std Error: 27.00 Plate: 11081 row: 06 column: C Seq primer: ACTGAGCGTCGTTTACACGCTGTGACTGAGGAAAAAC High quality sequence start: 98 High quality sequence stop: 630 POLYA-No.		
FEATURES			
source	location/Qualifiers		
	1..631		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/tissue_type="mixed"		
	/clone_lib="Full length cDNA from the Mammalian Gene Collection"		
	/note="Vector: mixed. The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"		
ORIGIN			
Alignment Scores:			
Score: No.:	2.24e-99	Length:	631
Percent Similarity:	1119.00	Matches:	208
	99.05%	Conservative:	0

Best Local Similarity:	99.05%	Mismatches:	2
Query Match:	74.01%	Indels:	0
DB:	7	Gaps:	0

US-09-598-982C-52 (1-275) x CV030374 (1-631)		
Oy	1 MetheusSerleuleuleuleuleualaleuProvalIeualaseratalatyalalapro	20
Dd	1 ATGCTGAGCCTGCTGCTGTGCCTCCGCTCTGGCGAGCCGGGCTACGGCCCCCT	60
Oy	21 AlaProValGlnalaLeuGlnGlnalaGlyTlavalglyGlnglnualaProArSser	40
Dd	61 GCCCAATGCCAGGCGCTTCGACGAAGCGGATATCGCGGGGTCAAGAAGCCCCAGAGNC	120
Oy	41 LysTrpProTrpGlnValSerLeuArgValAlArgAsparGlyTrpMetHisPheCysGly	60
Dd	121 AAGAGGCCCTGGCAGGTGAGCCTGAGATCGGCACCGAATACTGGAGCACTTGCGGG	180
Oy	61 GlySerleuleuleiSPROGINTRPValleThraIalAHiasCytleuGlyProAspVal	80
Dd	181 GGCTTCCTCATCCACCCCAGTGGGTCTGAACCAGCGGCGACTGCTCGGAGCCGAGCTC	240
Oy	81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyTYrgInaspGln	100
Dd	241 AAGATCTGGGCACACCTTCAGGGGTCAACTGGGGAGCAGCACCTCTACTACAGAGCAG	300
Oy	101 LeuLeuProValSerAargllelevalHisProGlnPheTyrllelglnThrGlyAla	120
Dd	301 CTGCTGCCGGTACAGCAAGATCATGTCTACCCACAGTTCTAACATCATCCAGACTGAGAGC	360
Oy	121 AspIleAlaLeuGlnGlnGlnGlnGlnProValasnIleSerSerArgValHisThrVal	140
Dd	361 GAATGCCCTGCTGGAGCTGGAGAGACCGGTGAACATCTTCAGCCCGGTTCACAGGCTC	420
Oy	141 MetHeuProProAlaSerGlnThrPheProProGlyMetProCystTrpValThrGlyTrp	160
Dd	421 ATGTGTGCCCCGTGCTGGAGACTTCCTCCCCGGGAGATGCGGTGATCGAGCTGG	480
Oy	161 GlysApValAspaAnaSpGluProLeuProProProPheProLeuLysGlnValLysVal	180
Dd	481 GGCATGTGACAAATGATGAGCCCTCCACCGCCATTTCCTCCCGAAGCAGGTGAAGTTC	540
Oy	181 ProIleMetGlnasnHistiCysAspAlaLysrYrHisLeuGlyAlaTyrrThGlyAsp	200
Dd	541 CCCATAATGAAAAACAATTGTGAGCANMAATACCACTTGCGGCTACACGGAGAC	600
Oy	201 AspValArgIlelelAArgspAspMetLeu	210
Dd	601 GAGCTCCGCATCATCTCGTAGCAGACTGCTG	630

RESULT 5	CD616760	673 bp	mRNA	linear	EST 12-JAN-2004
LOCUS	CD616760				
DEFINITION	56015240J1 FLP Homo sapiens cDNA, mRNA sequence.				
VERSION	CD616760				
KEYWORDS	CD616760.1 GI:40265024				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 673).				
AUTHORS	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.				
TITLE	Circular rapid amplification of cDNA ends for high-throughput				
	extension cloning of partial genes				
JOURNAL	Genomics 84 (1), 205-210 (2004)				
COMMENT	Contact: Fu GK				
	Incyte Genomics, Inc.				
	3160 Porter Dr., Palo Alto, CA 94304, USA				
	Tel.: 6508454102				
	Email: gfu@incyte.com.				
FEATURES					
source	I..673				
	Location/Qualifiers				

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

Alignment Scores:
Pred. No.: 4,31e-99 Length: 673
Score: 1116.50 Matches: 216
Percent Similarity: 96.00% Conservative: 0
Best Local Similarity: 96.00% Mismatches: 8
Query Match: 73.84% Indels: 4
DB: 6 Gaps: 0

US-09-598-982C-52 (1-275) x CD616760 (1-673)

QY 12 LeuAlaSerArgAlaTyrAlaAlaProAlaProValGlnAlaLeuGlnAlaGlylle 31
DB 2 CTGGGAGCGCGCGCTTACGCGCGCTGCGCCGATCCAGGCTGCGAGCAAGCGGATC 61
QY 32 ValGlyGlyGlnGlnAlaProArgSerlySTPProTIPGlnValSerleuArgValArg 51
DB 62 GTGGGGGAGTCAAGAGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
QY 52 AapaATGTTTTPMetHisPheCysGlyGlySerleuLeuHisProGlnTTPValleuThr 71
DB 122 GACCAATACATGATGACTTCTGCGGGGCTCTCTATCACCCTCCAGTGGTGTGAC 181
QY 72 AlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValGlnleuArg 91
DB 182 GCGGCGCACTGCTGGAGCCGAGACGTCAGATCTGGCACTCGAGGTGCACTGCGG 241
QY 92 GlnGlnHisLeuTyrTyrGlnAspGlnleuLeuProValSerArgIleIleValHisPro 111
DB 242 GAGCAGACACTTACTTACAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
QY 112 GlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnleuGlnProVal 131
DB 302 CAGTTCTTACATCATCAGACTGAGAGGATATCGCTGAGCTGAGAGAGAGAGAGAG 361
QY 132 AsnIleSerSerArgValHisThrValMetleuProProAlaSerGlnThrPheProPro 151
DB 362 AACATCTCCAGCGCGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
QY 152 GlyMetProCysTTPValThrGlyTTP-GlyAspValAspAspAspGlnProleuProPr 171
DB 422 GGGATGCGCTGCTGGGTCACTGGCTGGGGCGATGTGAGCAATGATGAGAGAGAG 481
QY 171 oPhePheProleuLysGlnValLysValProIleMetGlnAsnHisIleCysAspAlaLys 191
DB 482 GGAATTTTCCCTGAGACAGAGGTAAAGTCCCATTAAGGAAACCAATTTGTGAGAGCA 541
QY 191 sTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAspMetleuCy 211
DB 542 ATACCACTTTGGCGCTTACACGGAGACAGAGTCCGATCATTCGAGAGAGAGAGAG 601
QY 211 aaIaGlyAsnSerGlnArgAspSerCysAlaGlyAspSerGlyGlyProleuValCysAla 231
DB 602 TCGCGGAGACAG-CAGAGGAGATC-TGCAAGGGCGAGCTCTGAGGGGCTGTGCTTGAG 659
QY 231 sValaAsnGlyThr 235
DB 660 -GTGAATGGCACC 671

RESULT 6
CD616759/c 682 bp mRNA linear EST 12-JAN-2004
LOCUS
DEFINITION 56015240H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD616759
VERSION CD616759.1 GI:40265023
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
source location/qualifiers
1..682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:
Pred. No.: 2,56e-97 Length: 682
Score: 1098.50 Matches: 221
Percent Similarity: 97.37% Conservative: 1
Best Local Similarity: 96.93% Mismatches: 5
Query Match: 72.65% Indels: 6
DB: 6 Gaps: 0

US-09-598-982C-52 (1-275) x CD616759 (1-682)

QY 9 LeuProValLeuAlaSerArgAlaTyrAlaAlaProAlaProValGlnAlaLeuGln 28
DB 678 CTGCGCGGCTCTGGAGAC-CGCGCTTACGCGCGCTGCGCCGATCCAGGCTGAGCA 620
QY 29 AlaGlyIleValGlyGlyGlnGlnAlaProArgSerlySTPProTIPGlnValSerleu 48
DB 619 GCGGATATCGTCGGGGGTCAAGAGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 560
QY 49 ArgValArgAspArgTyrTTPMet-HisPheCysGlyGlySerleuIleHisProGlnThr 68
DB 559 AGAGTCCGAGCCAGTACTGATGATGACTTCTGCGGGGCTCTCCATCCAGCCAG-TG 501
QY 68 PValleuThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgVal 88
DB 500 GGTGCTGACCGCGGGGCACTGCTGGAGACCGAGCTCAAGATCTGGCACCTTCAAGGT 441
QY 88 IGlneuArgGlnGlnHisLeuTyrTyrGlnAspGlnleuLeuProValSerArgIleI 108
DB 440 GCACTGCGGGAGAGCACTCTTACTTACAGAGACAGCTGCTGCGAGAGAGATCAT 381
QY 108 eValHisProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnleuG 128
DB 380 CGTGACACCAAGATTCTTATCATTCACAGACTGAGAGCGGATATCGGCTGTGAGAGTGA 321
QY 128 uGlnProValAsnIleSerSerArgValHisThrValMetleuProProAlaSerGln 148
DB 320 GGAGCGCTGAAACATCTCCAGCGCGCTCCACAGGTCAATGCTGCGCTGTGAGAGAC 261
QY 148 PheProProGlyMetProCysTTPValThrGlyTTPGlyAspValAspAspAspGlnPr 168
DB 260 CTTCCCCCGGGAGATCGCTGCTGGGTACTGCTGGGGGCAATGTGAGAGAGAGAG 201
QY 168 oLeuProProProPheProleuLysGlnValLysValProIleMetGlnAsnHisIleCy 188
DB 200 CTTCCCAACGCAATTTCCCTGAGAGAGAGTGAAGTCCCATTAATGAGAAACCAATTG 141
QY 188 sAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAs 208
DB 140 TGAAGC-AAAATACCACTTGGCGCTTACACAGAGAGAGAGAGAGAGAGAGAGAGAG 82
QY 208 pMetleuCyAlaGlyAsnSerGlnArgAspSerCysAlaGlyAspSerGlyGlyProle 228

Db 81 CAGCTGTGTGCGGGAACGACGAGGAGGACTCTCGAAGGCGACTCTGAGAGCCCTTG 22
 QY 228 uValCysLysValAsnGlyThr 235
 Db 21 -GTCTGCAG-GTGAATGGCACCC 2
 RESULT 7
 CD672689 642 bp mRNA linear EST 24-JUN-2003
 LOCUS fgl5s06.5', mRNA sequence.
 DEFINITION fgl5s06.5', mRNA sequence.
 ACCESSION CD672689
 VERSION CD672689.1 GI:32174420
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 642)
 Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
 Expressed sequence tag analysis of adult human iris for the NEIbank
 project: steroid-response factors and similarities with retinal
 pigment epithelium
 Mol. Vis. 8 (4), 185-195 (2002)
 JOURNAL MEDLINE 22103462
 PUBMED 12107412
 COMMENT Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 15 row: a column: 06
 Seq primer: M13RP1 reverse primer (ABT).
 Location/Qualifiers
 1..642
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="fg15606"
 /tissue_type="Iris"
 /dev_stage="Adult"
 /lab_host="EMDHI0B"
 /clone_lib="Human Iris cDNA (Normalized): fg"
 /note="Organ: Eye; Vector: pCMVSPORT6; A human iris
 library (bx) was normalized by self-subtraction. One
 portion of double stranded plasmid DNA representing the
 library was linearized by NotI. This NotI digested library
 was used as a template for biotinylated RNA synthesis
 using SP6 RNA polymerase. Another portion of the double
 stranded plasmid library was converted to single-stranded
 circles in vitro using Gene II and Exonuclease III (Life
 Technologies). Single-stranded DNA (1 mg) was hybridized
 (60C 500) with 41 mg of Bio-RNA and vector blocking
 oligonucleotides. The hybridized Bio-RNA/ss-circles were
 removed by streptavidin:phenol extraction. EST analysis
 was performed on the library at the NIH Intramural
 Sequencing Center (NISC)."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,23e-95 length: 642
 Score: 1081.00 Matches: 198
 Percent Similarity: 95.75% Conservative: 5
 Best Local Similarity: 93.40% Mismatches: 9
 Query Match: 71.49% Indels: 0
 Gaps: 0
 DB: 6
 US-09-598-982C-52 (1-275) x CD672689 (1-642)

QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaPro 20
 Db 6 ATGCTGAATCTGCTGCTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 65
 QY 21 AlaProValGlnAlaLeuGlnGlnAlaGlyLeuValGlyGlnGlnAlaProArgSer 40
 Db 66 GCCCAAGCCAGAGCCCTGAGGAGTGGCAATGTTGGAGGTCAGAGAGCCCAAGAGCC 125
 QY 41 LysTrpProTyrGlnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGly 60
 Db 126 AAGTGGCCCTGCGACAGTACGCTGAGAGTCCGCGACCGAATACATGATCATTCTGGCGGG 185
 QY 61 GlySerLeuLeuHisProGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspVal 80
 Db 186 GGCTCCCTCATCCACCCCAAGAGTGGTGTGACCCGACGCGCATCTGCGAGACCGGACGCTC 245
 QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspGln 100
 Db 246 AAGGATCTGGCCGCTGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 305
 QY 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120
 Db 306 CTGCTGCGCGTACAGACGATCATCTGCACCCACAGCTTCTACACGCCCAAGATCGAGCG 365
 QY 121 AspIleAlaLeuLeuGlnLeuGlnGlnProValAsnIleSerSerArgValHisThrVal 140
 Db 366 GACATCGCCCTGCTGAGCTGAGAGAGCGGTGAACGCTCCAGCACGTCACACGCGTGC 425
 QY 141 MetLeuProProAlaSerGlnThrPheProProGlyMetProCysTyrValThrGlyTyr 160
 Db 426 GCCCTGCCCCCTGCTCGACAGACCTTCCCCCGGGAGAGCGGTGGGTGATCATCTGGCGG 485
 QY 161 GlyAspValAspAspAspGlnProLeuProProProPheProLeuLysGlnValLysVal 180
 Db 486 GCGCATGTGGACAATGATGAGGCGCTCCACCGCATTTCTCTGAACAGGTGAAGTTC 545
 QY 181 ProIleMetGlnAsnHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAsp 200
 Db 546 CCCATTAATGGAAMAACCAATTGTTGACGCAAAATCCACTTGGCGCTACACGGAGAGAC 605
 QY 201 AspValArgIleIleArgAspAspMetLeuCysAla 212
 Db 606 GACGTCCGATGCTCGTGAACACATGCTGTGTGC 641
 RESULT 8
 CF553058 806 bp mRNA linear EST 22-SEP-2003
 LOCUS AGENCOURT_15594982 NIH_MGC_183 Homo sapiens cDNA clone
 DEFINITION IMAGE:30529468 5', mRNA sequence.
 ACCESSION CF553058
 VERSION CF553058.1 GI:34889892
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 806)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Daniela S. Gerhardt, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgcgbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: NDAM617 row: b column: 05

Db 240 TATGGGACCAAGCTCTCTTTGAACCGGATGCTGTGACACCCCACTATTACAGGCC 299

Qy 117 GlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluProValAsnIleSerArg 136

Db 300 GAAGGTGGGCAACAGTGGCTGCTGGAGCTTGAAGTCCCTGTGATGCTCCACCCT 359

Qy 137 ValHisThrValMetLeuProAlaSerGluThrPheProProGlyMetProCysTrp 156

Db 360 ATCCACCCCATATCCCTGCCCCCTGGCTGGAGACTTCCCTCCCTGGAGCATGCTCTG 419

Qy 157 ValThrGlyThrGlyAspValAspAsnAspGluProLeuProProProPheProLeu 176

Db 420 GTACAGGGCTGGGGCAGCATTAATGAGAGCCCTCTCCACCTCTTAATCTCTGAAG 479

Qy 177 GluValIysValProIleMetGluAsnHisIleCysAspAlaIysTrpHisLeuGlyAla 196

Db 480 CAAGTGAAGTTCCTCATTTGGAAAAACAGCTGTGTGACCGGAATACCACTAGCCCTC 539

Qy 197 TyrThrGlyAspAspValAlaGlyIleIleArgAspAspMetLeuCysAlaGlyAsnSerGln 216

Db 540 TACACGGAGATGATTTTCCCATTTGTCATGATGACATGCTGTGTGTAATACAG 599

Qy 217 ArgAspSerCysIysGlyAspSerGlyGlyProLeuValCysIysValAsnGlyThrTrp 236

Db 600 AGAGACTCTCTGCAAGGCGCATTCAGGGGGCCTGCTGTGCAAGTGAAGGTACTCTG 659

Qy 237 LeuGlnAlaGlyValValSerTrp-AspGluGlyCysAlaGlnProAsnArgProGlyIle 256

Db 660 CTGACGAGCAGAGATGTGTGCTGCTGAGGTGAGGGCTGGCAGCCCAAGACGTGGCAT 719

Qy 256 eYrYrThrArg-ValThr-TyrTyrLeuAspTrpIleHis-HisTyrValProLys 273

Db 720 CTACACCCGGGGTGACATANTACTTAAGACTGATCCACGCTATGCTCTGAA 774

RESULT 10

LOCUS CD671891 635 bp mRNA linear EST 24-JUN-2003

DEFINITION fg08b10.y2 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone

ACCESSION CD671891

VERSION CD671891.1 GI:32173622

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 635)

AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.

TITLE Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

PROJECT Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium

Mol. Vis. 8 (4), 185-195 (2002)

JOURNAL MEDLINE 22103462

COMMENT 12107412

CONTACT: Mstow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 08 row: b column: 10

Seg primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1..635

/organism="Homo sapiens"

/mol_type="RNA"

/db_xref="taxon:9606"

/clone="fg08b10"

/tissue_type="Iris"

/dev_stage="Adult"

/lab_host="EMDHI0B"

/clone_lib="Human Iris cDNA (Normalized): fg"

/note="Organ: Eye; Vector: pCMVSPORT6; A human iris library (bx) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using Sp6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:

Pred. No.: 1,61e-91 Length: 635

Score: 1039.00 Matches: 191

Percent Similarity: 93.78% Conservative: 5

Best Local Similarity: 91.39% Mismatches: 13

Query Match: 68.72% Indels: 0

DB: 6 Gaps: 0

US-09-598-982C-52 (1-275) x CD671891 (1-635)

Qy 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaPro 20

Db 7 ATGCTGAATCTGCTGCTGCTGCGCTGCCGCTCGGGAGCGCGGCTTACCGGCCCT 66

Qy 21 AlaProValGlnAlaLeuGlnGlnAlaGlyIleValGlyGlyGlnAlaProArgSer 40

Db 67 GCCCAGGCGCAGGCCCTCGAGAGTGGCATGTCGGGGGTCAGAGAGCCGCCAGAGC 126

Qy 41 LysTrpProTrpGlnValSerLeuArgValAlaArgAspArgTyrTrpMetHisPheCysGly 60

Db 127 AAGTGGCCCTGGCAGAGTGAGCTGAGAGTCATGGCCCATCTGATGACACTTGTGCG 186

Qy 61 GlySerLeuIleHisProGlnTrpValLeuThrAlaAlaHisCysLeuGlyProAspVal 80

Db 187 GGCTCCCTCATCACCCCGAGGTGCTGCTCGAGGCGCATGCTGGAGCGGACGTC 246

Qy 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnHisLeuTyrTyrGlnAspGln 100

Db 247 AAGGATCTGCGCGCTCAGGGTGCACTGCGGAGAGACACTTACTACAGAGCCAG 306

Qy 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120

Db 307 CTGCTGCCGTGAGAGAGATCTGTGCAACCCGAGTCTACACCGCCAGATCGGAGCG 366

Qy 121 AspIleAlaLeuLeuGluLeuGluGluProValAsnIleSerSerArgValHisThrVal 140

Db 367 GACATCGCCCTCTGAGCTGAGAGAGCGCGGAGACGTCTCCAGCAGCATCCACGCGTC 426

Qy 141 MetLeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThrGlyTrp 160

Db 427 ACCCTGCCCCCTGCTCAGAGACTTCCCGCGGAGATGCGGTGCTGCTCACTGCTGG 486

Qy 161 GlyAspValAlaAspAsnAspGluProLeuProProProPheProLeuGlnValIysVal 180

Db 487 GGCAGTGTGACAAATGATGAGGCTCCCAACCGCATTTCTCTTAACAGAGTGAAGTTC 546

Qy 181 ProIleMetGluAsnHisIleCysAspAlaIysTyrHisLeuGlyAlaTyrThrGlyAsp 200

Db 547 CCATTAATGAAACCACTTTGTGACGCAAAATCCACTTTGGGCTTACAGCGGAGAC 606

Qy 201 AspValArgIleIleArgAspAspMet 209

Db 607 GACGTCCGATCGTCGTGACAGCATG 633

RESULT 11

BI413250

[illegible]

Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 433.

FEATURES

source

1. 589

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6036761"

/tissue_type="Insulinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="Human insulinoma"

/note="Organ: pancreas; Vector: pBluescript SK-; Site 1: XhoI; Site 2: EcoRI; Constructed with lambda ZapII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.:	2,51e-88	Length:	589
Score:	1006.00	Matches:	180
Percent Similarity:	95.85%	Conservative:	5
Best Local Similarity:	93.26%	Mismatches:	8
Query Match:	66.53%	Indels:	0
DB:	5	Gaps:	0

US-09-598-982c-52 (1-275) x BU071733 (1-589)

QY 79 AspValIysAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTYrTYrGln 98
Db 10 GAGCTGACAGATCTGGCCGCTCAGGGTGAACCTGGGAGCAGCAGCTTACTTACAG 69
QY 99 AsgGlnLeuLeuProValSerArgIleIleValHisProGlnPheTYrIleIleGlnThr 118
Db 70 GACCACCTGCTGCCGCTCAGCAGATCATCTGCACCCACAGTTCTTACACCGCCAGATC 129
QY 119 G1ValAspIleAlaLeuLeuGlnGlnGlnProValAsnIleSerArgValHis 138
Db 130 GAGGCGGACATCGCCCTGCTGAGCTGAGAGCCGCTGACATCTTCCAGCAGCTCAC 189
QY 139 ThrValMetLeuProProAlaSerGlnThrPheProProGlyMetProCysTrpValThr 158
Db 190 ACGGTCACTGCTGCCCTGCTCAGAGACCTTCCCCCGGGAGATGCGTGGGTCACT 249
QY 159 G1YTrpG1YAspValAspAsnAspGluProLeuProProPheProLeuLeuGlnVal 178
Db 250 GCGTGGGGCGATGTGACATGTAGCGCTCCACCGCATTTCTTGAAGCAGG 309
QY 179 LysValProIleMetGlnLeuHisIleCysAspAlaIleTYrHisLeuGlnValTYrThr 198
Db 310 AAGTCCCTCAATATGAAACCACTTTGTGACGCAAAATACCACTTGGCGCTTACAG 369
QY 199 G1YAspAspValArgIleIleArgAspAspMetLeuCysAlaG1YAsnSerGlnArgAsp 218
Db 370 GAGAGCAGATCGCGATCGTCCGTGACGATCTGTGTGCGCGGAAACCCGAGAGGAG 429
QY 219 SerCysLeuG1YAspSerG1YLeuProLeuValCysLeuValAsnG1YThrTrpLeuGln 238
Db 430 TCATGTCAGGGCAGCTCCGAGGGGCCCTGTGTGCAAGGTGATGCACTTGGCTGAG 489
QY 239 AlaG1YValValSerTrpAspG1YLeuValGlnProAsnArgProG1YIleTYrThr 258
Db 490 GCGGGGCTGCTCAGCTGGGGCGAGGCTGTGCGCAGCCCAACCGGGCTTGCATCTACAC 549

QY 259 ArgValIleTYrTYrLeuAspTrpIleHisIleTYrVal 271
Db 550 CGTGTCACTACTTGTGAGTGCATCCACCACATATGTC 588

RESULT 13

LOCUS

BG697540

DEFINITION

BG697540

811 bp

mRNA

linear EST 07-MAY-2001

Accession

BG697540

NCI_CGAP_Skn3 Homo sapiens

CDNA clone IMAGE:4803879 5',

Version

BG697540.1

GI:13963867

Keywords

EST.

Human sapiens (human)

Source

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Reference

NIH-MGC

http://mgs.nci.nih.gov/

1 (bases 1 to 811)

Mammalia; Euteleostomi; Primates; Carnivora; Homnidae; Homo.

Authors

Unpublished (1999)

Title

Unpublished (1999)

Journal

Unpublished (1999)

Comment

Contact: Robert Strausberg, Ph.D.

Text

Email: cgapbs-remail.nih.gov

Text

Tissue Procurement: James Cleaver, M.D.

Text

CDNA Library Preparation: Life Technologies, Inc.

Text

Sequencing by: Incyte Genomics, Inc.

Text

Clone distribution: MGC clone distribution information can be

Text

found through the I.M.A.G.E. Consortium/LNLN at:

Text

http://image.llnl.gov

Text

Plate: LNLN10700

Text

High quality sequence stop: 781.

FEATURES

source

1. 811

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4803879"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI CGAP Skn3"

/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NciI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.:	1,63e-86	Length:	811
Score:	989.50	Matches:	200
Percent Similarity:	77.41%	Conservative:	9
Best Local Similarity:	74.07%	Mismatches:	17
Query Match:	65.44%	Indels:	45
DB:	4	Gaps:	3

US-09-598-982c-52 (1-275) x BG697540 (1-811)

QY 1 MetLeuSerLeuLeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTYrAlaPro 20
Db 11 AAGTGAATATGCTCTGCTGCGCTGCCGCTGCGGAGCGCGCTTACAGCGGAC-CCT 69
QY 21 AlaProValGlnAlaLeuGlnGlnAlaG1YIleValG1YGlnGlnValProArgSer 40
Db 70 GCGCCAGCGCAGGCGCTCAGAGATGCGATCGTTGGGGGTCAAGAGCGCCCGCAGAGC 129
QY 41 LysTrpProTrpGlnValSerLeuArgValArgAspArgTYrTrpMetHisPheCysGly 60
Db 130 AAGTGGCCCTGACAGTGAAGCTTGAAGTCCAGGCCCATCTGATGCACTTCTGCGAG 189
QY 61 G1YSerLeuIleHisProGlnTrpValLeuThrAlaAlaHisCysLeuG1YProAspVal 80
Db 190 GCGTCCCTCATTCACCCCAAGTGGGTGTGACCGGAGCGCATGCTGTGAGACCGGACGTC 249
QY 81 LysAspLeuAlaThrLeuArgValGlnLeuArgGlnHisLeuTYrTYrGlnAspGln 100


```

Db 250 AAGATCTGCGCCGCTGAGGTCGACCTGCGGAGCAGACCTTACTACAGGACCG 309
Qy 101 LeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAla 120
Db 310 CTGCTGCGCGGTGAGGATCATCTGTCACCCACAGATTCTACACCGCCAGATCCGAGCG 369
Qy 121 AApIleAlaLeuLeuGluLeuGluProValAsnIleSerSerArgValHisThrVal 140
Db 370 GACATGCGCTCTGAGCTGAGGAGCCGGTGAAGTCTCCAGCCACGTCACACGCTC 429
Qy 141 MetLeuProProAlaSerGluThrPheProGlyMetProCysTyrValThrGlyTyr 160
Db 430 ACCCTGCGCCCTGCTCTGAGACCTTCCCCCGGGAGATCCCTGCTGGTCACTGGCTG 489
Qy 161 GlyAspValAspAsnAsp----- 166
Db 490 GGGCATGTGACATGATGTGGTCTGGGAGACAGTGAAGTGGGGCCAGGGTCTTAGCC 549
Qy 166 ----- 166
Db 550 ACAGCCGACGCCCTGGGCTCCTGTGGCTCCAGGTGGGGGTGGCCCGCCCTCTGAG 609
Qy 167 ---GluProLeuPro-----Pro-ProPheProLeuLysGlnValIleVal 180
Db 610 GGTGACCTCTTCCCCACCTGACAGAGCGCTCCACGCACTTCTCTGAAAGCAGGTAGGT 669
Qy 180 LProIleMetGluAsnHisIleCysAspAlaLysTyrHis-LeuGlyAlaTyrThrGlyAla 200
Db 670 CCCCATTAATGAAACCAACATTTGTGAAGGCAAGATACACTGGGCGGCTTACAGGGAG 729
Qy 200 SpAspValArgIleIleLeuArgAspAsp-MetLeuCybAlaGlyAsnSerGlnArgAspSer 219
Db 730 AGCAGCTGCGCATGCTCGCTGACGAACATGCTGTGTGGGAGAACCCGAG--GACTCA 786
Qy 220 CysLysGlyAspSerGlyLysPro 227
Db 787 TCCCAAGCGCATCTCCGAGGGGCC 810

RESULT 14
LOCUS BU787772 581 bp mRNA linear EST 11-OCT-2002
DEFINITION i03c08.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6128247
5' similar to SW:TRYS_HUMAN P20231 BETA-TRYPTASE PRECURSOR ;, mRNA
sequence.
ACCESSION BU787772.1 GI:23835713
VERSION BU787772
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 581)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemisha, I., Scease, M., Bresciani, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marra, M., Page, D., Wylie, T., Martin, J., Bliscain, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: i034c08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a

```

clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40RP from GIBCO
 High quality sequence stop: 427.
 Location/Qualifiers
 1. 581

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6128247"
 /lab_host="DH10B (phage-resistant)"
 /issue="Insulinoma"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
 XhoI; Site 2: EcoRI; Constructed with lambda ZapI system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further
 information on this library (Metabolism Division, Permut
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:
 Pred. No.: 1.01e-83 Length: 581
 Score: 959.00 Matches: 176
 Percent Similarity: 93.72% Conservative: 3
 Best Local Similarity: 92.15% Mismatches: 12
 Query Match: 63.43% Indels: 0
 DB: 5 Gaps: 0

US-09-598-982C-52 (1-275) x BU787772 (1-581)

```

Qy 5 LeuLeuLeuAlaLeuProValLeuAlaSerArgAlaTyrAlaAlaProAlaProValGln 24
Db 8 CTGCTGCTGGCGGCTGCGCCCTCTGCGAGCGCGGCTTACGCGGCCCTCGCCGAGGACG 67
Qy 25 AlaLeuGlnGlnAlaGlyTleValGlyGlnGlnAlaProArgSerLysTyrProTyr 44
Db 68 GCCCTGCGAGGAGTGGGATGCTGGGGGTGAGAGGCGCCGAGAGCAAGTGGCCCTG 127
Qy 45 GlnValSerLeuArgValArgAspArgTyrTrpMetHisPheCysGlySerLeuIle 64
Db 128 CAGGTGAGCTGAGAGTTCACGCGCCCACTGATGACCTTCTGGGGGCTCCCTATTC 187
Qy 65 HisProGlnTyrValLeuThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAla 84
Db 188 CACCCCGAGTGGGTCTGACCCGAGCGGACGCTGCGGAGCGGAGCTCAAGATCTGGCC 247
Qy 248 GCCCTGAGGAGTGAACCTGCGGAGCAGACCTTACTACTACAGGACCAAGCTCTCGCGGTC 307
Db 85 ThrLeuArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProVal 104
Qy 248 GCCCTGAGGAGTGAACCTGCGGAGCAGACCTTACTACTACAGGACCAAGCTCTCGCGGTC 307
Db 105 SerArgIleIleValHisPheProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeu 124
Qy 308 AGCAGGATCATCTGTCACCCACAGTTTACACCGCCGAGATCGAGCGGACATGCGCTG 367
Db 125 LeuGluLeuGluGluProValAsnIleSerSerArgValHisThrValMetLeuProPro 144
Qy 368 CTGAGAGCTGAGAGAGCCGGTACGCTCCAGCCACGTCACAGGTCACCTGCCCTC 427
Db 145 AlaSerGluThrPheProGlyMetProCysTyrValThrGlyTyrGlyAspValAsp 164
Qy 428 GCTTCAGAGACCTTCCCCCGGGAGATCGGTGCTGAGTCACTGGCTGGGGGAGATGTGAC 487
Db 165 AsnAspGluProLeuProProPheProLeuLysGlnValLysValProIleMetGly 184
Qy 488 AATGATGAGCCCTCCACCGCCCATTTCTGTGAAGGAGGTGAAGTCCCATTAATGAA 547
Db 185 AsnHisIleCysAspAlaLysTyrHisLeuGly 195

```

Db 548 AACCACTTTGTGACGCAAAATACCACTTGGC 580

RESULT 15
BG542089 736 bp mRNA linear EST 03-APR-2001
LOCUS 602571309F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695458 5',
DEFINITION mRNA sequence.
ACCESSION BG542089
VERSION BG542089.1 GI:13534322
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 736)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LNCM1521 row: b column: 03
High quality sequence stop: 725.
Location/Qualifiers

FEATURES

1..736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4695458"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1b="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCATG-(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 4.79e-80 Length: 736
Score: 923.00 Matches: 199
Percent Similarity: 85.95% Conservative: 9
Best Local Similarity: 82.23% Mismatches: 24
Query Match: 61.04% Indels: 12
DB: 4 Gaps: 1

US-09-598-982c-52 (1-275) x BG542089 (1-736)

Qy 1 MetLeuSerLeuLeuLeuAlaLeuProValLeuAlaSerArg-AtATyrAlaAlaPr 20
Db 24 ATCTGATATCTGCTGCTGCGCGCTGCCGCTGCGAGCCTGCGCGCGCC 83
Qy 20 ca1aProValGlnAlaLeuGlnAlaGlyIleValGlyGlnGlnAlaProArgse 40
Db 84 TGCCCAAGGCGAGCCCTGCGAGGAGGAGCATGTTGGGGGTCAAGAGGCCCGCCAGAG 143
Qy 40 rLysTrpTrpTrpGlnValSerLeuAlaArgAspArgTyrTrpMetHisPheCysG1 60
Db 144 CAAGTGAGCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 203
Qy 60 yGlySerLeuIleHisProGlnTrpValLeuThrAlaIleHisCysLeuG1yProAspVa 80

Db 204 GAGCTCCCTCATCCACCCCAAGTGGTGTGACCCGAGCGACCTGCGGAGCCGAGCT 263
Qy 80 llyAspLeuAlaThrLeuArgValGlnLeuArgGlnGlnHisLeuTyrTyrGlnAspG1 100
Db 264 CAAGGATCTGCGCGCCCTCAGGGGTGCACTGGGGAGAGACCTCTACTACAGAGACA 323
Qy 100 nLeuLeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAl 120
Db 324 GCTGTGCGCGGTCAAGAGATCATGTGACCCAGAGTTCTACACCGCCAGATCGAGAGC 383
Qy 120 aAspIleAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
Db 384 GGAACATCCCGCTGCTGAGAGCTGAGAGACCGGTGAAGTCTTCAACACCTGACAGGT 443
Qy 140 lMetLeuProProAlaSerGlnThrPheProPro-GlyMetProCysTrpValThrGlyT 160
Db 444 CACCTGCGCCCTGCTGAGAGACCTTCCCGCGGGGATGCGGCTGCGGTCACTGAGCT 503
Qy 160 TrGlyAspValAsp-AspAspGlnUProLeuProProPheProLeuLysGlnVal-Ly 179
Db 504 GGGGCGATGTGACCAATGATGAGGCGCT-CCAGCGCATTTCTTCTGAAGCAGGTGAA 562
Qy 179 sValProIleMetGlnAsnHisIleCysAspAlaLysTyrHisLeuGlyAla-TyrThrG 199
Db 563 GGTCCCATATGCAAAACCACTTTGTGACGCAAAATPACACCTTGGGGCTTAACAGG 622
Qy 199 lYAspAsp-ValArgIle-----IleArgAspMetLeuCysAlaGlyAsnSerGln 216
Db 623 GAGACGAAGGTCCGATTCGTCCGGTGAACGACAT-TGCTGTTGGCGGGAAACCCGG 681
Qy 217 ArgAspSerCysLeuGly-AspSer-GlyGlyProLeuValCysLeuVal 232
Db 682 AGGAGCTATGCGCAGGGCGGAGCTCGGAGGGCGCCCTGCTGTCAGAGGTG 731

Search completed: August 30, 2005, 17:42:35
Job time : 3128 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2005, 23:29:16 ; Search time 114 Seconds
(without alignments)
947.848 Million cell updates/sec

Title: US-09-598-982c-52

Perfect score: 1512
Sequence: 1 MSLSLALLPVLASRAYAP.....ITYRTYLDVIMHHVPRKP 275

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1512	100.0	275	14	US-10-117-323-36 Sequence 36, Appl
2	1512	100.0	275	15	US-10-352-684A-46 Sequence 46, Appl
3	1414	93.5	275	15	US-10-287-226-90 Sequence 90, Appl
4	1411	93.3	275	15	US-10-287-226-92 Sequence 92, Appl
5	1411	93.3	275	16	US-10-723-860-2690 Sequence 2690, Ap
6	1411	93.3	275	18	US-10-756-149-5451 Sequence 5451, Ap
7	1405	92.9	275	10	US-09-813-432-44 Sequence 44, Appl
8	1405	92.9	275	15	US-10-352-684A-48 Sequence 48, Appl
9	1405	92.9	275	15	US-10-174-364-44 Sequence 44, Appl
10	1405	92.9	275	15	US-10-246-583-44 Sequence 44, Appl
11	1405	92.9	275	15	US-10-287-226-94 Sequence 94, Appl

12	1405	92.9	275	16	US-10-689-832-44 Sequence 44, Appl
13	1401	92.7	691	15	US-10-275-505-13 Sequence 13, Appl
14	1386.5	91.7	272	14	US-10-117-323-40 Sequence 40, Appl
15	1373	90.8	243	11	US-09-789-210-69 Sequence 69, Appl
16	1360	89.9	264	14	US-10-131-409-104 Sequence 104, App
17	1360	89.9	264	15	US-10-139-854-104 Sequence 104, App
18	1360	89.9	264	15	US-10-150-813-104 Sequence 104, App
19	1360	89.9	264	15	US-10-150-811-104 Sequence 104, App
20	1355.5	89.7	279	15	US-10-287-226-88 Sequence 88, Appl
21	1349	89.2	266	14	US-10-131-409-84 Sequence 84, Appl
22	1349	89.2	266	15	US-10-139-854-84 Sequence 84, Appl
23	1349	89.2	266	15	US-10-150-813-84 Sequence 84, Appl
24	1349	89.2	266	15	US-10-150-811-84 Sequence 84, Appl
25	1324	87.6	256	14	US-10-131-409-92 Sequence 92, Appl
26	1324	87.6	256	15	US-10-139-854-92 Sequence 92, Appl
27	1324	87.6	256	15	US-10-150-813-92 Sequence 92, Appl
28	1324	87.6	256	15	US-10-150-811-92 Sequence 92, Appl
29	1313	86.8	254	14	US-10-131-409-74 Sequence 74, Appl
30	1313	86.8	254	15	US-10-139-854-74 Sequence 74, Appl
31	1313	86.8	254	15	US-10-150-813-74 Sequence 74, Appl
32	1313	86.8	254	15	US-10-150-811-74 Sequence 74, Appl
33	1186	78.4	231	10	US-09-898-837A-52 Sequence 52, Appl
34	1134	75.0	310	15	US-10-275-505-8 Sequence 8, Appl1
35	1133	74.9	276	14	US-10-117-323-35 Sequence 35, Appl
36	1118	73.9	273	15	US-10-028-248A-63 Sequence 63, Appl
37	1118	73.9	273	15	US-10-107-782-63 Sequence 63, Appl
38	1113	73.6	276	15	US-10-311-955-3 Sequence 3, Appl1
39	1108	73.3	242	17	US-10-80-988-27 Sequence 27, Appl
40	1103	72.9	273	15	US-10-028-248A-64 Sequence 64, Appl
41	1103	72.9	273	15	US-10-107-782-64 Sequence 64, Appl
42	1094	72.4	252	10	US-09-813-432-42 Sequence 42, Appl
43	1094	72.4	252	15	US-10-174-364-42 Sequence 42, Appl
44	1094	72.4	252	15	US-10-246-583-42 Sequence 42, Appl
45	1094	72.4	252	16	US-10-689-832-42 Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-10-117-323-36
; Sequence 36, Application US/10117323
; Publication No. US2003054993A1
; GENERAL INFORMATION:
; APPLICANT: Rancourt, Derrick E.
; APPLICANT: Rancourt, Susan L.
; TITLE OF INVENTION: Implantation Sertine Proteinases
; FILE REFERENCE: 03337-005
; CURRENT APPLICATION NUMBER: US/10/117,323
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/281,724
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/294,736
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/350,962
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-323-36

Query Match 100.0%; Score 1512; DB 14; Length 275;
Best Local Similarity 100.0%; Pred. No. 4.5e-130;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MSLSLALLPVLASRAYAPVQALQAGIVGQEARSRMPQVSLRVRDRYMMFFCG 60
|||||
Db 1 MSLSLALLPVLASRAYAPVQALQAGIVGQEARSRMPQVSLRVRDRYMMFFCG 60
|||||

```
QY 61 GSLIHQWVLTAAHCLGPDVKDLATLRVQLREOHLTYDDQLPVSRIIVHPOFYIIQTGA 120
|
|
|
Db 61 GSLIHQWVLTAAHCLGPDVKDLATLRVQLREOHLTYDDQLPVSRIIVHPOFYIIQTGA 120
|
|
|
QY 121 DIALLELEBPVNISSRVHTVMTLPPASETFPPGMPGKVTGMDVNDDEPLPPFPPLKQYKV 180
|
|
|
Db 121 DIALLELEBPVNISSRVHTVMTLPPASETFPPGMPGKVTGMDVNDDEPLPPFPPLKQYKV 180
|
|
|
QY 181 PIMENHICDAKYHLAGYTGDDVRIIRDMLCAGNSQSDCKGDSGGPLVCYKVGWTWLOAG 240
|
|
|
Db 181 PIMENHICDAKYHLAGYTGDDVRIIRDMLCAGNSQSDCKGDSGGPLVCYKVGWTWLOAG 240
|
|
|
QY 241 VVSWDEGCAQPNRPGLIYTRVITYLDMIHVYVKKP 275
|
|
|
Db 241 VVSWDEGCAQPNRPGLIYTRVITYLDMIHVYVKKP 275
|
|
|
```

RESULT 2

```
US-10-352-684A-46
/ Sequence 46, Application US/10352684A
/ Publication No. US20030215452A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals Inc.
/ APPLICANT: Cartoll, Joseph M.
/ APPLICANT: Healy, Aileen
/ APPLICANT: Kelly, Nadine S.
/ APPLICANT: Kelly, Louise M.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
/ TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
/ TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
/ TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
/ FILE REFERENCE: MP102-019P1RNOINIM
/ CURRENT APPLICATION NUMBER: US/10/352,684A
/ PRIOR FILING DATE: 2003-01-28
/ PRIOR APPLICATION NUMBER: US 60/354,333
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: US 60/360,258
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/364,476
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/375,626
/ PRIOR FILING DATE: 2002-04-26
/ PRIOR APPLICATION NUMBER: US 60/386,494
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: US 60/390,965
/ PRIOR FILING DATE: 2002-06-24
/ PRIOR APPLICATION NUMBER: US 60/392,480
/ PRIOR FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: US 60/394,128
/ PRIOR FILING DATE: 2002-07-03
/ PRIOR APPLICATION NUMBER: US 60/399,783
/ PRIOR FILING DATE: 2002-07-31
/ PRIOR APPLICATION NUMBER: US 60/403,221
/ PRIOR FILING DATE: 2002-08-13
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 46
/ LENGTH: 275
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-352-684A-46
```

```
Query Match 100.0%; Score 1512; DB 15; Length 275;
Best Local Similarity 100.0%; Pred No. 4,5e-130;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MSTLLILALPVLTASRAYPAPVQALQAGIGVGGDEAPRSKMPWQVSLRVDRYVMWHFGG 60
|
|
|
Db 1 MSTLLILALPVLTASRAYPAPVQALQAGIGVGGDEAPRSKMPWQVSLRVDRYVMWHFGG 60
|
|
|
QY 61 GSLIHQWVLTAAHCLGPDVKDLATLRVQLREOHLTYDDQLPVSRIIVHPOFYIIQTGA 120
|
|
|
```

```
Db 61 GSLIHQWVLTAAHCLGPDVKDLATLRVQLREOHLTYDDQLPVSRIIVHPOFYIIQTGA 120
|
|
|
QY 121 DIALLELEBPVNISSRVHTVMTLPPASETFPPGMPGKVTGMDVNDDEPLPPFPPLKQYKV 180
|
|
|
Db 121 DIALLELEBPVNISSRVHTVMTLPPASETFPPGMPGKVTGMDVNDDEPLPPFPPLKQYKV 180
|
|
|
QY 181 PIMENHICDAKYHLAGYTGDDVRIIRDMLCAGNSQSDCKGDSGGPLVCYKVGWTWLOAG 240
|
|
|
Db 181 PIMENHICDAKYHLAGYTGDDVRIIRDMLCAGNSQSDCKGDSGGPLVCYKVGWTWLOAG 240
|
|
|
QY 241 VVSWDEGCAQPNRPGLIYTRVITYLDMIHVYVKKP 275
|
|
|
Db 241 VVSWDEGCAQPNRPGLIYTRVITYLDMIHVYVKKP 275
|
|
|
```

RESULT 3

```
US-10-287-226-90
/ Sequence 90, Application US/10287226
/ Publication No. US20040086875A1
/ GENERAL INFORMATION:
/ APPLICANT: Agee, Michele L.,
/ APPLICANT: Alsobrook, John P.,
/ APPLICANT: Berghs, Constance,
/ APPLICANT: Boldog, Ference,
/ APPLICANT: Burgess, Catherine E.,
/ APPLICANT: Chant, John S.,
/ APPLICANT: Chaudhuri, Amitabha,
/ APPLICANT: DiPippo, Vincent A.,
/ APPLICANT: Edinger, Shlomit R.,
/ APPLICANT: Eisen, Andrew,
/ APPLICANT: Ellerman, Karen,
/ APPLICANT: Gangolli, Esha A.,
/ APPLICANT: Gorman, Linda,
/ APPLICANT: Gerlach, Valerie,
/ APPLICANT: Ji, Weizhen,
/ APPLICANT: Kekuda, Ramesh,
/ APPLICANT: Khramtsov, Nikolai,
/ APPLICANT: Li, Li,
/ APPLICANT: Malyanakar, Uriel M.,
/ APPLICANT: MacDougall, John R.,
/ APPLICANT: Mezes, Peter S. E.,
/ APPLICANT: Miller, Charles E.,
/ APPLICANT: Millet, Isabelle,
/ APPLICANT: Ooi, Chean Eng,
/ APPLICANT: Ort, Tatiana,
/ APPLICANT: Padigara, Muralidhara,
/ APPLICANT: Patnayan, Meera,
/ APPLICANT: Rastelli, Luca,
/ APPLICANT: Rieger, Daniel K.,
/ APPLICANT: Rothenberg, Mark E.,
/ APPLICANT: Shenoy, Suresh G.,
/ APPLICANT: Spaderna, Steven K.,
/ APPLICANT: Spyrek, Kimberley A.,
/ APPLICANT: Taubert, Jr., Raymond J.,
/ APPLICANT: Vernier, Corine A.M.,
/ APPLICANT: Zernusen, Bryan D.,
/ APPLICANT: Zhong, Mei
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-480C
/ CURRENT APPLICATION NUMBER: US/10/287,226
/ PRIOR FILING DATE: 2002-11-04
/ PRIOR APPLICATION NUMBER: 60/334,421
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,392
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/360,148
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: 60/364,000
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/404,821
/ PRIOR FILING DATE: 2002-08-20
/ PRIOR APPLICATION NUMBER: 60/334,526
```

```

; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: Curation version 0.1
; SEQ ID NO 90
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-287-226-90

```

```

Query Match      93.5%; Score 1414; DB 15; Length 275;
Beet Local Similarity 92.7%; Pred. No. 4,3e-121;
Matches 255; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

```

```

QY 1 MSLTLLALPVLASRAVAAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMMHFCG 60
DB 1 MSLTLLALPVLASRAVAAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMMHFCG 60
QY 61 GSLHPQWVLTAAHCLGPDVQDLATLRVQLREOHLYYQDQLPVSRIIVHPQFYIIOTGA 120
DB 61 GSLHPQWVLTAAHCLGPDVQDLATLRVQLREOHLYYQDQLPVSRIIVHPQFYIIOTGA 120
QY 121 DIALLEEBPVNIVSSRVHTVWLPPASETFPPGMPGMCWTGWDVNDDEPLPPFPKQKV 180
DB 121 DIALLEEBPVNIVSSRVHTVWLPPASETFPPGMPGMCWTGWDVNDDEPLPPFPKQKV 180
QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNSQDSCKGSGPLVCKVNGTWTLOAG 240
DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNTRBDSCKGSGPLVCKVNGTWTLOAG 240
QY 241 VVSMDEGCAQPNRPGLITRTVYTYLDWIHHYVPKKP 275
DB 241 VVSMDEGCAQPNRPGLITRTVYTYLDWIHHYVPKKP 275

```

RESULT 4

```

US-10-287-226-92
; Sequence 92, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Bsha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khramtsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyanek, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.,
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,

```

```

; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernier, Corine A.M.,
; APPLICANT: Zernusen, Bryan D.,
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: Curation version 0.1
; SEQ ID NO 92
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-287-226-92

```

```

Query Match      93.3%; Score 1411; DB 15; Length 275;
Beet Local Similarity 92.4%; Pred. No. 8.1e-121;
Matches 254; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

```

```

QY 1 MSLTLLALPVLASRAVAAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMMHFCG 60
DB 1 MSLTLLALPVLASRAVAAPAPVQALQAGIVGQGEAPRSKMPQVSLRVDRYMMHFCG 60
QY 61 GSLHPQWVLTAAHCLGPDVQDLATLRVQLREOHLYYQDQLPVSRIIVHPQFYIIOTGA 120
DB 61 GSLHPQWVLTAAHCLGPDVQDLATLRVQLREOHLYYQDQLPVSRIIVHPQFYIIOTGA 120
QY 121 DIALLEEBPVNIVSSRVHTVWLPPASETFPPGMPGMCWTGWDVNDDEPLPPFPKQKV 180
DB 121 DIALLEEBPVNIVSSRVHTVWLPPASETFPPGMPGMCWTGWDVNDDEPLPPFPKQKV 180
QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNSQDSCKGSGPLVCKVNGTWTLOAG 240
DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDDMLCAGNTRBDSCKGSGPLVCKVNGTWTLOAG 240
QY 241 VVSMDEGCAQPNRPGLITRTVYTYLDWIHHYVPKKP 275
DB 241 VVSMDEGCAQPNRPGLITRTVYTYLDWIHHYVPKKP 275

```

RESULT 5

```

US-10-723-860-2690
; Sequence 2690, Application US/10723860

```

```
/ Publication No. US20040253606A1
/ GENERAL INFORMATION:
/ APPLICANT: Aziz, Natasha
/ APPLICANT: Ginsburg, Wendy M.
/ APPLICANT: Zlotnick, Albert
/ TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
/ FILE REFERENCE: 05882.0193.NPUS01
/ CURRENT APPLICATION NUMBER: US/10/723,860
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: 60/429,739
/ PRIOR FILING DATE: 2002-11-26
/ NUMBER OF SEQ ID NOS: 8393
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2690
/ LENGTH: 275
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-723-860-2690
```

```
Query Match          93.3%; Score 1411; DB 16; Length 275;
Best Local Similarity 92.4%; Pred. No. 8,1e-121;
Matches 254; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 MSLLLALPVLASRAVAAPAPVQALQOAGIVGQGEAPRSKMPQVSLRVDRYMMHFCG 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNLILLALPVLASRAVAAPAPGQALQRVGIVGQGEAPRSKMPQVSLRVHGPYMMHFCG 60

QY 61 GSLIHPOWVLTAAHCLGPDVKDLATLRVQLREQHLYYQDQLPVSRITVHPQFYITQGA 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GSLIHPOWVLTAAHCGPVDKDLAALRVQLREQHLYYQDQLPVSRITVHPQFYITQIGA 120

QY 121 DIALLEBEPVNISSRVHTVMTLPPASSETPPGMPGCVWTGMDVNDDEPLPPFPPLKQVY 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DIALLEBEPVNVSSHHTVTLPPASSETPPGMPGCVWTGMDVNDNERLPPFPPLKQVY 180

QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQDSCKGDSGGLVCKVNGTWMQAG 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 PIMENHICDAKXHLGAYTGDDVRIIVDDMLCAGNTRSDSCQDSGGLVCKVNGTWMQAG 240

QY 241 VVSMDEGCAQPNRPGIYTRVITYLLDMTHHYVPKKP 275
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VVSMDEGCAQPNRPGIYTRVITYLLDMTHHYVPKKP 275
```

RESULT 6

```
US-10-756-149-5451
/ Sequence 5451, Application US/10756149
/ Publication No. US20050181375A1
/ GENERAL INFORMATION:
/ APPLICANT: Aziz, Natasha
/ APPLICANT: Zlotnick, Albert
/ TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
/ FILE REFERENCE: file
/ CURRENT APPLICATION NUMBER: US/10/756,149
/ CURRENT FILING DATE: 2004-01-12
/ NUMBER OF SEQ ID NOS: 5818
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 5451
/ LENGTH: 275
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-756-149-5451
```

```
Query Match          93.3%; Score 1411; DB 18; Length 275;
Best Local Similarity 92.4%; Pred. No. 8,1e-121;
Matches 254; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 MSLLLALPVLASRAVAAPAPVQALQOAGIVGQGEAPRSKMPQVSLRVDRYMMHFCG 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNLILLALPVLASRAVAAPAPGQALQRVGIVGQGEAPRSKMPQVSLRVHGPYMMHFCG 60
```

```
QY 61 GSLIHPOWVLTAAHCLGPDVKDLATLRVQLREQHLYYQDQLPVSRITVHPQFYITQGA 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GSLIHPOWVLTAAHCGPVDKDLAALRVQLREQHLYYQDQLPVSRITVHPQFYITQIGA 120

QY 121 DIALLEBEPVNISSRVHTVMTLPPASSETPPGMPGCVWTGMDVNDDEPLPPFPPLKQVY 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DIALLEBEPVNVSSHHTVTLPPASSETPPGMPGCVWTGMDVNDERLPPFPPLKQVY 180

QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQDSCKGDSGGLVCKVNGTWMQAG 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 PIMENHICDAKXHLGAYTGDDVRIIVDDMLCAGNTRSDSCQDSGGLVCKVNGTWMQAG 240

QY 241 VVSMDEGCAQPNRPGIYTRVITYLLDMTHHYVPKKP 275
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VVSMDEGCAQPNRPGIYTRVITYLLDMTHHYVPKKP 275
```

RESULT 7

```
US-09-813-432-44
/ Sequence 44, Application US/09813432
/ Publication No. US20030148485A1
/ GENERAL INFORMATION:
/ APPLICANT: Taupier Jr., Raymond J
/ APPLICANT: Majumder, Kamud
/ APPLICANT: Spaderna, Steven K
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Mezes, Peter S
/ APPLICANT: Vernet, Corine A. M.
/ TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
/ FILE REFERENCE: 15966-729
/ CURRENT APPLICATION NUMBER: US/09/813,432
/ CURRENT FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/190,835
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: 60/190,768
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: 60/190,972
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 60/191,199
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 60/191,947
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: 60/192,665
/ PRIOR FILING DATE: 2000-03-28
/ PRIOR APPLICATION NUMBER: 60/192,657
/ PRIOR FILING DATE: 2000-03-28
/ PRIOR APPLICATION NUMBER: 60/192,984
/ PRIOR FILING DATE: 2000-03-28
/ PRIOR APPLICATION NUMBER: 60/192,664
/ PRIOR FILING DATE: 2000-03-28
/ PRIOR APPLICATION NUMBER: 60/192,836
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: 60/193,843
/ PRIOR FILING DATE: 2000-03-31
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 44
/ LENGTH: 275
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-813-432-44
```

```
Query Match          92.9%; Score 1405; DB 10; Length 275;
Best Local Similarity 92.0%; Pred. No. 2,9e-120;
Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
```

```
QY 1 MSLLLALPVLASRAVAAPAPVQALQOAGIVGQGEAPRSKMPQVSLRVDRYMMHFCG 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNLILLALPVLASRAVAAPAPGQALQRVGIVGQGEAPRSKMPQVSLRVHGPYMMHFCG 60

QY 61 GSLIHPOWVLTAAHCLGPDVKDLATLRVQLREQHLYYQDQLPVSRITVHPQFYITQGA 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GSLIHPOWVLTAAHCGPVDKDLAALRVQLREQHLYYQDQLPVSRITVHPQFYITQIGA 120
```

QY 121 DIALLELEBPVNISRRVHTVWLPPASSETPPGMPGCVTGWGDVNDDEPLPPFPFLKQYKV 180
Db 121 DIALLELEBPVNVSSHVHTVTLPPASSETPPGMPGCVTGWGDVNDDEPLPPFPFLKQYKV 180
QY 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNSORDSCGDSGGPLVCYKNGTWTLOAG 240
Db 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNTRRDS CGDSGGPLVCYKNGTWTLOAG 240
QY 241 VVSMDEGCAQPNRPGIYTRVTVYLLDMTHHYVPKKP 275
Db 241 VVSMDEGCAQPNRPGIYTRVTVYLLDMTHHYVPKKP 275

RESULT 8

US-10-352-684A-48
; Sequence 48, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Kelly, Nadine S.
; APPLICANT: Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28058, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; FILE REFERENCE: MP102-019PRNOMNIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-352-684A-48

Query Match 92.9%; Score 1405; DB 15; Length 275;
Best Local Similarity 92.0%; Pred. No. 2.9e-120;
Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSLILLALPVLASRAVYAAPAVQALQAGIVGGEAPRSKMPQVSLRVRDRYMHFCG 60
Db 1 MNTULLALPVLASRAVYAAPAVQALQAGIVGGEAPRSKMPQVSLRVRDRYMHFCG 60
QY 61 GSLIHQWVLTAAHCLGPDVQDLATLRVQLREOHLTYDQDLIPVSRIVHPOFYITQGA 120
Db 61 GSLIHQWVLTAAHCLGPDVQDLATLRVQLREOHLTYDQDLIPVSRIVHPOFYITQGA 120

QY 121 DIALLELEBPVNISRRVHTVWLPPASSETPPGMPGCVTGWGDVNDDEPLPPFPFLKQYKV 180
Db 121 DIALLELEBPVNVSSHVHTVTLPPASSETPPGMPGCVTGWGDVNDDEPLPPFPFLKQYKV 180
QY 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNSORDSCGDSGGPLVCYKNGTWTLOAG 240
Db 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNTRRDS CGDSGGPLVCYKNGTWTLOAG 240
QY 241 VVSMDEGCAQPNRPGIYTRVTVYLLDMTHHYVPKKP 275
Db 241 VVSMDEGCAQPNRPGIYTRVTVYLLDMTHHYVPKKP 275

RESULT 9

US-10-174-364-44
; Sequence 44, Application US/10174364
; Publication No. US20030216308A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; FILE REFERENCE: 15966-729CIP2
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; CURRENT APPLICATION NUMBER: US/10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-364-44

Query Match 92.9%; Score 1405; DB 15; Length 275;
Best Local Similarity 92.0%; Pred. No. 2.9e-120;
Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSLILLALPVLASRAVYAAPAVQALQAGIVGGEAPRSKMPQVSLRVRDRYMHFCG 60
Db 1 MNTULLALPVLASRAVYAAPAVQALQAGIVGGEAPRSKMPQVSLRVRDRYMHFCG 60
QY 61 GSLIHQWVLTAAHCLGPDVQDLATLRVQLREOHLTYDQDLIPVSRIVHPOFYITQGA 120
Db 61 GSLIHQWVLTAAHCLGPDVQDLATLRVQLREOHLTYDQDLIPVSRIVHPOFYITQGA 120
QY 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNSORDSCGDSGGPLVCYKNGTWTLOAG 240
Db 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNTRRDS CGDSGGPLVCYKNGTWTLOAG 240
QY 241 VVSMDEGCAQPNRPGIYTRVTVYLLDMTHHYVPKKP 275

```
Db      241 VVSMGSCAQNRPGLYTRVYLLDWIHHVPPKP 275
RESULT 10
US-10-246-583-44
; Sequence 44, Application US/10246583
; Publication No. US200405862A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-583-44

Query Match      92.9%; Score 1405; DB 15; Length 275;
Best Local Similarity 92.0%; Pred. No. 2,9e-120;
Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY      1 MSLLLLALPVLASRAVAPAPVQALQAGIVGGQAPRSKMPWQVSLVRDYMWHFPG 60
Db      1 MNLVLLALPVLASRAVAPAPVQALQAGIVGGQAPRSKMPWQVSLVRHGPYMHFPG 60
QY      61 GSLIHPOWVLTAAHCLGPDVXDATLRVQLREOHLVYDQLLPSRIIVHPQYIIQTGA 120
Db      61 GSLIHPOWVLTAAHCLGPDVXDALRLVQLREOHLVYDQLLPSRIIVHPQYIIQTGA 120
QY      121 DIALLEBEPVNISSRVHTYMLRPASSTPPGMPCWNTGKGVNDDEPLPPPLKQVY 180
Db      121 DIALLEBEPVNISSRVHTYMLRPASSTPPGMPCWNTGKGVNDDEPLPPPLKQVY 180
QY      181 PIWENHICQAKYHLGAVTGDDVRIIRDDMLCAGNSORDSCGSGSLVCKVNGTWLQAG 240
Db      181 PIWENHICQAKYHLGAVTGDDVRIIRDDMLCAGNSORDSCGSGSLVCKVNGTWLQAG 240
QY      241 VVSMDEGCAQPNRPGLYTRVYLLDWIHHVPPKP 275
Db      241 VVSMGSCAQNRPGLYTRVYLLDWIHHVPPKP 275

RESULT 11
US-10-287-226-94
; Sequence 94, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
```

```
APPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Bergs, Constance,
APPLICANT: Boldog, Ference,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: DiPippo, Vincent A.,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Eisen, Andrew,
APPLICANT: Ellerman, Karen,
APPLICANT: Gangolli, Esba A.,
APPLICANT: Gorman, Linda,
APPLICANT: Gerlach, Valerie,
APPLICANT: Ji, Weizhen,
APPLICANT: Kekuda, Ramesh,
APPLICANT: Khramtsov, Nikolai,
APPLICANT: Li, Li,
APPLICANT: MaYankar, Uriel M.,
APPLICANT: MacDougall, John R.,
APPLICANT: Mezes, Peter S.,
APPLICANT: Miller, Charles E.,
APPLICANT: Millet, Isabelle,
APPLICANT: Ooi, Chean Eng,
APPLICANT: Orc, Tatiana,
APPLICANT: Padigaru, Muralidhara,
APPLICANT: Patuturajan, Meera,
APPLICANT: Rastelli, Luca,
APPLICANT: Rieger, Daniel K.,
APPLICANT: Rothenberg, Mark E.,
APPLICANT: Shenoy, Suresh G.,
APPLICANT: Spaderna, Steven K.,
APPLICANT: Spytek, Kimberley A.,
APPLICANT: Taupier, Jr., Raymond J.,
APPLICANT: Vernet, Corine A.M.,
APPLICANT: Zernusen, Bryan D.,
APPLICANT: Zhong, Mei,
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 94
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-94

Query Match      92.9%; Score 1405; DB 15; Length 275;
Best Local Similarity 92.0%; Pred. No. 2,9e-120;
Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
```


QY 1 MLSTLLTALPTLASRAVAAPAPVQALQAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
DB 1 MLNLLTLLALPTLASRAVAAPAPGQALQAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
QY 61 GSLIHPQWVLTAAACIGPVDVQDLATLRVQLEOHLYYQDQLLPVSRILVHPQFYIIQGA 120
DB 61 GSLIHPQWVLTAAACIGPVDVQDLATLRVQLEOHLYYQDQLLPVSRILVHPQFYIIQGA 120
QY 121 DIALLEBEPVNISRRVHTVTLPPASSETPPGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
DB 121 DIALLEBEPVNISRRVHTVTLPPASSETPPGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDMDLCAQNSQSDSCGSGPLVCVKNGTWLQAG 240
DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDMDLCAQNSQSDSCGSGPLVCVKNGTWLQAG 240
QY 241 VVSWDEGCAQPNRPQITRTVYTYLDWIMHHYVPPKP 275
DB 241 VVSWDEGCAQPNRPQITRTVYTYLDWIMHHYVPPKP 275

RESULT 12

US-10-689-832-44
; Sequence 44, Application US/10689832
; Publication No. US2004012180A1
; GENERAL INFORMATION:
; APPLICANT: Majumder, Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729DIV1
; CURRENT APPLICATION NUMBER: US/10/689,832
; PRIOR APPLICATION NUMBER: 09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-832-44

Query Match 92.9%; Score 1405; DB 16; Length 275;
Best Local Similarity 92.0%; Pred. No. 2,9e-120;
Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MLSTLLTALPTLASRAVAAPAPVQALQAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
DB 1 MLNLLTLLALPTLASRAVAAPAPGQALQAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
QY 61 GSLIHPQWVLTAAACIGPVDVQDLATLRVQLEOHLYYQDQLLPVSRILVHPQFYIIQGA 120
DB 61 GSLIHPQWVLTAAACIGPVDVQDLATLRVQLEOHLYYQDQLLPVSRILVHPQFYIIQGA 120

QY 121 DIALLEBEPVNISRRVHTVTLPPASSETPPGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
DB 121 DIALLEBEPVNISRRVHTVTLPPASSETPPGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDMDLCAQNSQSDSCGSGPLVCVKNGTWLQAG 240
DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDMDLCAQNSQSDSCGSGPLVCVKNGTWLQAG 240
QY 241 VVSWDEGCAQPNRPQITRTVYTYLDWIMHHYVPPKP 275
DB 241 VVSWDEGCAQPNRPQITRTVYTYLDWIMHHYVPPKP 275

RESULT 13

US-10-275-505-13
; Sequence 13, Application US/10275505
; Publication No. US20040081961A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELGEMAN, Angelo M.; LAL, Preeti G.
; APPLICANT: HARALIA, April J.A.; PATTERSON, Chandra
; APPLICANT: WALIA, Narinder K.; KEARNEY, Liam
; APPLICANT: TRIBOUTIEY, Catherine M.; KHAN, Farrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda; ELIOTT, Vicki S.
; APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.
; APPLICANT: YANG, Junning; HERNANDEZ, Roberto
; APPLICANT: POLICKY, Jennifer L.; LU, Dying Aina M.
; APPLICANT: REDDY, Roopa M.; YUE, Henry
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0085 USN
; CURRENT APPLICATION NUMBER: US/10/275,505
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/US01/14651
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/209,402
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/207,477
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/205,803
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/203,566
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/202,082
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7472460CD1
US-10-275-505-13

Query Match 92.7%; Score 1401; DB 15; Length 691;
Best Local Similarity 92.0%; Pred. No. 2e-119;
Matches 253; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 MLSTLLTALPTLASRAVAAPAPVQALQAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
DB 1 MLNLLTLLALPTLASRAVAAPGQALQAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 68
QY 61 GSLIHPQWVLTAAACIGPVDVQDLATLRVQLEOHLYYQDQLLPVSRILVHPQFYIIQGA 120
DB 61 GSLIHPQWVLTAAACIGPVDVQDLATLRVQLEOHLYYQDQLLPVSRILVHPQFYIIQGA 128
QY 121 DIALLEBEPVNISRRVHTVTLPPASSETPPGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
DB 121 DIALLEBEPVNISRRVHTVTLPPASSETPPGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 188

```

QY      181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNSQSDSGGSLVCKVNGTWLQAG 240
      |||
Db      189 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNTRDSCGSDSGSLVCKVNGTWLQAG 248
QY      241 VVSMDEGCAQPNRPGIYTRVYTYLLDMTHHVPKPP 275
      |||
Db      249 VVSMDEGCAQPNRPGIYTRVYTYLLDMTHHVPKPP 283

```

RESULT 14

```

US-10-117-323-40
; Sequence 40, Application US/10117323
; Publication No. US20030054993A1
; GENERAL INFORMATION:
; APPLICANT: Rancourt, Derrick E.
; APPLICANT: Rancourt, Susan L.
; APPLICANT: O'Sullivan, Colleen M.
; TITLE OF INVENTION: Implantation Serine Proteinases
; FILE REFERENCE: 033337-005
; CURRENT APPLICATION NUMBER: US/10/117,323
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/281,724
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/294,736
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/350,962
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mouse
US-10-117-323-40

```

```

Query Match      91.7%; Score 1386.5; DB 14; Length 272;
Best Local Similarity 91.9%; Pred. No. 1.4e-118;
Matches 251; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

```

```

QY      3 SLLLLLPVLASRAVAAAPAVQALQAGIVGGGEAPRSKMPQVSLRVDRYMHFCGSS 62
      |||
Db      1 NULLLLPVLASRAVAAAPAGQALQGVIVGGGEAPRSKMPQVSLRVHGPYMHFCGSS 60
QY      63 LHPQVNLTAHCLGPDVCDLATLRVQLREQLHYDDQLPVSRIIVHPQFYIIQGADI 122
      |||
Db      61 LHPQVNLTAHCLGPDVCDLATLRVQLREQLHYDDQLPVSRIIVHPQFYIIQGADI 119
QY      123 ALLELEPNVNISSRVHTVMLPPASETFPPGMPQVTKGVDNDDEPLPPFPLKQVKPI 182
      |||
Db      120 ALLELEPNVNISSRVHTVTLPPASETFPPGMPQVTKGVDNDDEPLPPFPLKQVKPI 179
QY      183 MENHICDAKYHLGAYTGDDVRIIRDMLCAGNSQSDSGGSLVCKVNGTWLQAGV 242
      |||
Db      180 MENHICDAKYHLGAYTGDDVRIIRDMLCAGNTRDSCGSDSGGSLVCKVNGTWLQAGV 239
QY      243 SMDEGCAQPNRPGIYTRVYTYLLDMTHHVPKPP 275
      |||
Db      240 SMDEGCAQPNRPGIYTRVYTYLLDMTHHVPKPP 272

```

RESULT 15

```

US-09-789-210-69
; Sequence 69, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:

```

```

; APPLICANT: COHEN, MAURICE
; COLEPITS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLAS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.

```

```

; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-789-210-69

```

```

Query Match      90.8%; Score 1373; DB 11; Length 245;
Best Local Similarity 100.0%; Pred. No. 2.1e-117;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      31 IVGGGEAPRSKMPQVSLRVDRYMHFCGSLIHPQVNLTAHCLGPDVCDLATLRVQL 90
      |||
Db      1 IVGGGEAPRSKMPQVSLRVDRYMHFCGSLIHPQVNLTAHCLGPDVCDLATLRVQL 60
QY      91 REQLHYDDQLPVSRIIVHPQFYIIQGADIALLELEPNVNISSRVHTVMLPPASETFP 150
      |||
Db      61 REQLHYDDQLPVSRIIVHPQFYIIQGADIALLELEPNVNISSRVHTVMLPPASETFP 120
QY      151 PMPQVTKGVDNDDEPLPPFPLKQVKPIIMENHICDAKYHLGAYTGDDVRIIRDML 210
      |||
Db      121 PMPQVTKGVDNDDEPLPPFPLKQVKPIIMENHICDAKYHLGAYTGDDVRIIRDML 180
QY      211 CAGNSQSDSGGSLVCKVNGTWLQAGVSMDEGCAQPNRPGIYTRVYTYLLDMTHH 270
      |||
Db      181 CAGNSQSDSGGSLVCKVNGTWLQAGVSMDEGCAQPNRPGIYTRVYTYLLDMTHH 240
QY      271 VPKPP 275
      |||
Db      241 VPKPP 245

```

```

Search completed: August 27, 2005, 23:41:06
Job time : 115 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2005, 23:22:30 ; Search time 63 Seconds
(without alignments)
325.849 Million cell updates/sec

Title: US-09-598-982C-52
Perfect score: 1512
Sequence: 1 MSLSLLLALPVLASRAVAAP.....ITYRVTYLDWIMHHVPRKP 275

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1512	100.0	275	2	US-09-016-366A-17 Sequence 17, Appl
2	1512	100.0	275	2	US-08-978-404B-12 Sequence 12, Appl
3	1402	92.7	273	2	US-09-016-366A-19 Sequence 19, Appl
4	1402	92.7	273	2	US-08-978-404B-14 Sequence 14, Appl
5	1400	92.6	274	2	US-09-016-366A-21 Sequence 21, Appl
6	1400	92.6	274	2	US-08-978-404B-16 Sequence 16, Appl
7	1394	92.2	267	2	US-09-016-366A-23 Sequence 23, Appl
8	1394	92.2	267	2	US-08-978-404B-18 Sequence 18, Appl
9	1394	92.2	267	4	US-09-917-254-101 Sequence 101, App
10	1373	90.8	245	3	US-08-944-483-69 Sequence 69, Appl
11	1284	84.9	245	3	US-09-079-970A-6 Sequence 6, Appl
12	1284	84.9	245	4	US-09-601-318-1 Sequence 1, Appl
13	1284	84.9	249	4	US-09-079-970A-5 Sequence 5, Appl
14	1277	84.5	244	4	US-09-601-318-4 Sequence 4, Appl
15	1277	84.5	244	4	US-09-601-318-5 Sequence 5, Appl
16	1277	84.5	244	4	US-09-601-318-6 Sequence 6, Appl
17	1277	84.5	244	4	US-09-601-318-7 Sequence 7, Appl
18	1277	84.5	244	4	US-09-601-318-8 Sequence 8, Appl
19	1133	74.9	276	2	US-09-016-366A-15 Sequence 15, Appl
20	1133	74.9	276	2	US-08-978-404B-21 Sequence 21, Appl
21	1109.5	73.1	270	2	US-08-978-404B-8 Sequence 8, Appl
22	1105	73.1	273	2	US-08-978-404B-6 Sequence 6, Appl
23	1105	73.1	274	2	US-08-978-404B-5 Sequence 5, Appl
24	820	54.2	190	3	US-08-845-998-4 Sequence 4, Appl
25	820	54.2	190	3	US-09-206-537-4 Sequence 4, Appl
26	820	54.2	190	3	US-09-430-854-4 Sequence 4, Appl
27	816	54.0	190	2	US-08-845-998-6 Sequence 6, Appl

28	816	54.0	190	3	US-09-206-537-6 Sequence 6, Appl
29	816	54.0	190	3	US-09-430-854-6 Sequence 6, Appl
30	566.5	45.4	269	2	US-08-978-404B-10 Sequence 10, Appl
31	572.5	37.9	290	4	US-09-386-653A-7 Sequence 7, Appl
32	555	36.7	315	4	US-09-386-653A-9 Sequence 9, Appl
33	553.5	36.6	284	4	US-09-387-375-7 Sequence 7, Appl
34	553.5	36.6	284	4	US-10-041-400A-7 Sequence 7, Appl
35	553.5	36.6	284	4	US-10-042-091A-7 Sequence 7, Appl
36	535	35.4	316	4	US-09-387-375-9 Sequence 9, Appl
37	535	35.4	316	4	US-10-041-400A-9 Sequence 9, Appl
38	535	35.4	316	4	US-10-042-091A-9 Sequence 9, Appl
39	530.5	35.1	317	4	US-09-386-629-7 Sequence 7, Appl
40	530.5	35.1	317	4	US-09-907-794A-263 Sequence 263, App
41	530.5	35.1	317	4	US-09-905-125A-263 Sequence 263, App
42	530.5	35.1	317	4	US-09-902-775A-263 Sequence 263, App
43	530.5	35.1	317	4	US-09-906-700-263 Sequence 263, App
44	530.5	35.1	317	4	US-09-903-603A-263 Sequence 263, App
45	530.5	35.1	317	4	US-09-904-920A-263 Sequence 263, App

ALIGNMENTS

RESULT 1
US-09-016-366A-17
Sequence 17, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plummer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-366A-17
Query Match 100.0%; Score 1512; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 8.3e-153;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLLALPVLASRAYAAPAPVQALQAGIVGGQAPRSKMPWQVSLRVDRYMMHFCG 60
DB 1 MSLLLALPVLASRAYAAPAPVQALQAGIVGGQAPRSKMPWQVSLRVDRYMMHFCG 60
QY 61 GSLIHPOWVLTAAHCLGPDVNDLATLRVQLREOHLYYQDQLPVSRILVHPQFYIIQTGA 120
DB 61 GSLIHPOWVLTAAHCLGPDVNDLATLRVQLREOHLYYQDQLPVSRILVHPQFYIIQTGA 120
QY 121 DIALLEBEPVNISSRVHTVMLPPASETFPPGMPCWVTGMDVNDDEPLPPFPPLKQKV 180
DB 121 DIALLEBEPVNISSRVHTVMLPPASETFPPGMPCWVTGMDVNDDEPLPPFPPLKQKV 180
QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQSDSCGDSGGLVCKVNGTWLQAG 240
DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQSDSCGDSGGLVCKVNGTWLQAG 240
QY 241 VVSWDEGCAQPNRPGLYTRVTYYLDMIHYYVPKRP 275
DB 241 VVSWDEGCAQPNRPGLYTRVTYYLDMIHYYVPKRP 275

RESULT 2

US-08-978-404B-12
/ Sequence 12, Application US/08978404B
/ Patent No. 5968782
/ GENERAL INFORMATION:
/ APPLICANT: Stevens, Richard L.
/ TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
/ TITLE OF INVENTION: FIBRINOGEN
/ NUMBER OF SEQUENCES: 74
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02210-2211
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/978,404B
/ FILING DATE: 25-NOV-97
/ CLASSIFICATION: 435
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 60/032,354
/ FILING DATE: 04-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/7090
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 275 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: NO. 5968782e
US-08-978-404B-12

Query Match 100.0%; Score 1512; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 8,3e-153;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLLLALPVLASRAYAAPAPVQALQAGIVGGQAPRSKMPWQVSLRVDRYMMHFCG 60
DB 1 MSLLLALPVLASRAYAAPAPVQALQAGIVGGQAPRSKMPWQVSLRVDRYMMHFCG 60

QY 61 GSLIHPOWVLTAAHCLGPDVNDLATLRVQLREOHLYYQDQLPVSRILVHPQFYIIQTGA 120
DB 61 GSLIHPOWVLTAAHCLGPDVNDLATLRVQLREOHLYYQDQLPVSRILVHPQFYIIQTGA 120
QY 121 DIALLEBEPVNISSRVHTVMLPPASETFPPGMPCWVTGMDVNDDEPLPPFPPLKQKV 180
DB 121 DIALLEBEPVNISSRVHTVMLPPASETFPPGMPCWVTGMDVNDDEPLPPFPPLKQKV 180
QY 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQSDSCGDSGGLVCKVNGTWLQAG 240
DB 181 PIMENHICDAKXHLGAYTGDDVRIIRDMLCAGNSQSDSCGDSGGLVCKVNGTWLQAG 240
QY 241 VVSWDEGCAQPNRPGLYTRVTYYLDMIHYYVPKRP 275
DB 241 VVSWDEGCAQPNRPGLYTRVTYYLDMIHYYVPKRP 275

RESULT 3

US-09-016-366A-19
/ Sequence 19, Application US/09016366A
/ Patent No. 5955431
/ GENERAL INFORMATION:
/ APPLICANT: Stevens, Richard L.
/ APPLICANT: Huang, Chifu
/ TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
/ TITLE OF INVENTION: INHIBITORS
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02210-2211
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,366A
/ FILING DATE: January 30, 1998
/ CLASSIFICATION: 530
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 60/037,090
/ FILING DATE: 05-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/7093
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 273 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-016-366A-19

Query Match 92.7%; Score 1402; DB 2; Length 273;
Best Local Similarity 92.3%; Pred. No. 4,4e-141;
Matches 252; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
QY 3 SLLLLALPVLASRAYAAPAPVQALQAGIVGGQAPRSKMPWQVSLRVDRYMMHFCG 62
DB 1 MSLLLALPVLASRAYAAPAPVQALQAGIVGGQAPRSKMPWQVSLRVDRYMMHFCG 60
QY 63 LIHPQWVLTAAHCLGPDVNDLATLRVQLREOHLYYQDQLPVSRILVHPQFYIIQTGADI 122

Db 61 LIHPQWVLTAAHCVGPVDKDLAALRVLREQHLYYQDQLPVSRIIVHPQFYTAQIGADI 120
QY ALLELEEVNIVSSRHVTWMLPPASSETPPGMPGCVTGMGVDVNDERLPPFPFLKQVVP1 182
Db 123 ALLELEEVNIVSSRHVTWMLPPASSETPPGMPGCVTGMGVDVNDERLPPFPFLKQVVP1 180
QY 121 ALLELEEVNIVSSRHVTWMLPPASSETPPGMPGCVTGMGVDVNDERLPPFPFLKQVVP1 180
QY 183 MENNICAKYHLGATYGDVRIIRDDMLCAGNSORDSCGDSGGPLVCKVNGTWLQAGV 242
Db 181 MENNICAKYHLGATYGDVRIIRDDMLCAGNTRDSCGDSGGPLVCKVNGTWLQAGV 240
QY 243 SWDEGCAQPNRPGIYTRVTTYLLDWMHHYVPPKP 275
Db 241 SWDEGCAQPNRPGIYTRVTTYLLDWMHHYVPPKP 273

RESULT 4
US-08-978-404B-14
; Sequence 14, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 5968782
; US-08-978-404B-14

Query Match 92.7%; Score 1402; DB 2; Length 273;
Best Local Similarity 92.3%; Pred. No. 4,4e-141;
Matches 252; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 3 LILLIALPVLASRAVAPAPVOLAQAGIVGQBA PRSKMPQVSLRVDRYMMHFCGGS 62
Db 1 LILLIALPVLASRAVAPAPVOLAQAGIVGQBA PRSKMPQVSLRVDRYMMHFCGGS 60
QY 63 LIHPQWVLTAAHCVGPVDKDLAALRVLREQHLYYQDQLPVSRIIVHPQFYTAQIGADI 122
Db 61 LIHPQWVLTAAHCVGPVDKDLAALRVLREQHLYYQDQLPVSRIIVHPQFYTAQIGADI 120
QY 123 ALLELEEVNIVSSRHVTWMLPPASSETPPGMPGCVTGMGVDVNDERLPPFPFLKQVVP1 182

Db 121 ALLELEEVNIVSSRHVTWMLPPASSETPPGMPGCVTGMGVDVNDERLPPFPFLKQVVP1 180
QY 183 MENNICAKYHLGATYGDVRIIRDDMLCAGNSORDSCGDSGGPLVCKVNGTWLQAGV 242
Db 181 MENNICAKYHLGATYGDVRIIRDDMLCAGNTRDSCGDSGGPLVCKVNGTWLQAGV 240
QY 243 SWDEGCAQPNRPGIYTRVTTYLLDWMHHYVPPKP 275
Db 241 SWDEGCAQPNRPGIYTRVTTYLLDWMHHYVPPKP 273

RESULT 5
US-09-016-366A-21
; Sequence 21, Application US/09016366A
; Patent No. 5953431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-016-366A-21

Query Match 92.6%; Score 1400; DB 2; Length 274;
Best Local Similarity 92.0%; Pred. No. 7.2e-141;
Matches 252; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 2 LILLIALPVLASRAVAPAPVOLAQAGIVGQBA PRSKMPQVSLRVDRYMMHFCGGS 61
Db 1 LILLIALPVLASRAVAPAPVOLAQAGIVGQBA PRSKMPQVSLRVDRYMMHFCGGS 60
QY 62 SLIHPQWVLTAAHCVGPVDKDLAALRVLREQHLYYQDQLPVSRIIVHPQFYTAQIGADI 121
Db 61 SLIHPQWVLTAAHCVGPVDKDLAALRVLREQHLYYQDQLPVSRIIVHPQFYTAQIGADI 120
QY 122 ALLELEEVNIVSSRHVTWMLPPASSETPPGMPGCVTGMGVDVNDERLPPFPFLKQVVP1 181
Db 121 ALLELEEVNIVSSRHVTWMLPPASSETPPGMPGCVTGMGVDVNDERLPPFPFLKQVVP1 180

QY	Db	QY	Db
182	181	242	241
IMENHICDACYHGAATYGDVRIIRDDMCAANSORDCKSGSGPLVCKXNGTWLQAGV	IMENHICDACYHGAATYGDVRIIRDDMCAENTRRDSQGGSSGPLVCKXNGTWLQAGV	VSWDEGCAQPNRGITRYTRVLYLDMTHHHVPPKP	VSMGEGCAQPNRGITRYTRVLYLDMTHHHVPPKP

```

1      RESULT 6
2      US-08-978-404B-16
3      : Sequence 16, Application US/08978404B
4      : Patent No. 5968782
5      : GENERAL INFORMATION:
6      : APPLICANT: Stevens, Richard L.
7      : TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
8      : TITLE OF INVENTION: FIBRINOGEN
9      : NUMBER OF SEQUENCES: 74
10     : CORRESPONDENCE ADDRESS:
11     : ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
12     : STREET: 600 Atlantic Avenue
13     : CITY: Boston
14     : STATE: MA
15     : COUNTRY: U.S.A.
16     : ZIP: 02210-2211
17     : COMPUTER READABLE FORM:
18     : MEDIUM TYPE: Diskette
19     : COMPUTER: IBM Compatible
20     : OPERATING SYSTEM: DOS
21     : SOFTWARE: FastSeq for Windows Version 2.0
22     : CURRENT APPLICATION DATA:
23     : APPLICATION NUMBER: US/08/978,404B
24     : FILING DATE: 25-NOV-97
25     : CLASSIFICATION: 435
26     : PRIOR APPLICATION DATA:
27     : APPLICATION NUMBER: 60/032,354
28     : FILING DATE: 04-DEC-1996
29     : ATTORNEY/AGENT INFORMATION:
30     : NAME: Plumer, Elizabeth R.
31     : REGISTRATION NUMBER: 36,637
32     : REFERENCE/DOCKET NUMBER: B0801/7090
33     : TELECOMMUNICATION INFORMATION:
34     : TELEPHONE: 617-720-3500
35     : TELEFAX: 617-720-2441
36     : TELEX:
37     : INFORMATION FOR SEQ ID NO: 16:
38     : SEQUENCE CHARACTERISTICS:
39     : LENGTH: 274 amino acids
40     : TYPE: amino acid
41     : STRANDEDNESS: single
42     : TOPOLOGY: linear
43     : MOLECULE TYPE: No. 5968782e
44     : US-08-978-404B-16

```

Query Match	92.6%	Score 1400;	DB 2;	Length 274;
Best Local Similarity	92.0%	Pred. No. 7.2e-11;		
Matches 252; Conservative	8;	Mismatches 14;	Indels 0;	Gaps 0

QY	2	LSLTLALPLTASRAAALPAVOLQOAGI VGGGAPSPSKPMOWSLVLRGRYMHFCGG	61
		1	1
Db	1	1LNLTLALPLTASRAAALPAFGOLQORVGI VGGGAPSPSKPMOWSLVLRVGPYMHFCGG	60
QY	62	SLIHPQWVLTAAHCLGPDVKDLATLURVOLREOHLVYQDOLLVPSKLIIVHPQFYLIQCGAD	121
Db	61	SLIHPQWVLTAAHCVGPDVKDLAALRYQRLREGHLVYQDOLLVPSKLIIVHPQFYTAQCGAD	120
QY	122	1ALLLEIEEPVNISSRVHTWMLPPASSTFPPGMPGCVTGMGDVNDDELPPEPLKQYKVP	181
		1	1
Db	121	1ALLLEIEEPKVSSSHVHTVTLPPASSTFPPGMPGCVTGMGDVNDDELRPEPPLKQYKVP	180
QY	182	1MENH1CDAKYH1GATYGDVRI1IRDDM1CAANSQRDCKSDSGEPLCYKNGTWLQAGV	241
Db	181	1MENH1CDAKYH1GATYGDVRI1VRDDM1CAANTRRDSCQSGSGEPLCYKNGTWLQAGV	240

Qy 242 VSWDEGCAQPNNRPGIYTRVITYLLDWIHIVPKKP 275
| | | | | | | | | | | | | | | | | | | | |
Db 241 VSWGEGCAQPNRPGLYTRVITYLLDWHIVPCKP 274

RESULT 7
 US-09-016-366A-23
 Sequence 23, Application US/09016366A
 Patent No. 5955431
 GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 APPLICANT: Huang, Chifu
 TITLE OF INVENTION: MASH CELL PROTEASE PEPTIDE
 TITLE OF INVENTION: INHIBITORS
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,366A
 FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037,090
 FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7093
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-016-366A-23

Query Match	92.2%;	Score 1394;	DB 2;	Length 267;
Best Local Similarity	93.3%;	Pred. No. 3e-140;		
Matches 249;	Conservative	7;	Mismatches 11;	Indels 0;
			Gaps	0

QY 9 LPTLASRAVAAPARVQALCOAGIVGGGAPSPSKMPMOWSLRVRORYMHCCGSLIHPQW 68

Db 1 LPTLASRAVAAPARVQALQIRGIVGGGAPSPSKMPMOWSLRVRRYMHCCGSLIHPQW 60

QY 69 ULTAACCLGPDYKDLATLRVQLREHLLYYOQLPVSRILYHPQYIILQIGADLALLE 128

Db 61 ULTAACCVGPDYKDLAALRVQLREHLLYYOQLPVSRILYHPQYIILQIGADLALLE 120

QY 129 EPVNISSRHVTMLPEASIEPPGMPCWMTQMGVDNDELRPEFPFLQYKQVIMENHTIC 188

Db 121 EPKVASHVHTLTLPPEASIEPPGMPCWMTQMGVDNDELRPEFPFLQYKQVIMENHTIC 180

QY 189 DAKYHIGATGVDVYIIRDDMLCAENSNRDSCKXDSGSGRLPYCKYNGTWLQAGVSNDEGC 248

Db 181 DAKYHIGATGVDVYIIRDDMLCAENITKSDSCQDSGGLYCKYNGTWLQAGVSNDEGC 240

QY 249 AQPENRPGIYTRVYLLDMLHHVPPKP 275

DB 241 AQPNRPGIYTRVTVYLDWIHHYVPPKP 267

RESULT 8
US-08-978-404B-18

/ Sequence 18, Application US/08978404B

/ Patent No. 5968782

/ GENERAL INFORMATION:

/ APPLICANT: Stevens, Richard L.

/ TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES

/ TITLE OF INVENTION: FIBRINOGEN

/ NUMBER OF SEQUENCES: 74

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

/ STREET: 600 Atlantic Avenue

/ CITY: Boston

/ STATE: MA

/ COUNTRY: U.S.A.

/ ZIP: 02210-2211

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette

/ OPERATING SYSTEM: DOS

/ SOFTWARE: FastSeq for Windows Version 2.0

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/978,404B

/ FILING DATE: 25-NOV-97

/ CLASSIFICATION: 435

/ PRIORITY APPLICATION DATA:

/ APPLICATION NUMBER: 60/032,354

/ FILING DATE: 04-DEC-1996

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Plumer, Elizabeth R.

/ REGISTRATION NUMBER: 36,637

/ REFERENCE/DOCKET NUMBER: B0801/7090

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 617-720-3500

/ TELEFAX: 617-720-2441

/ INDEX:

/ INFORMATION FOR SEQ ID NO: 18:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 267 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: No. 5968782e

US-08-978-404B-18

Query Match 92.2%; Score 1394; DB 2; Length 267;

Best Local Similarity 93.3%; Pred. No. 3e-140; Mismatches 11; Indels 0; Gaps 0;

Matches 249; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

DB 9 LPTLASRAVAAPAPVQALQAGIVGGQAPRSKMPQVSLRVDRYMMHFCGSLIHPQW 68
1 LPTLASRAVAAPAPVQALQAGIVGGQAPRSKMPQVSLRVDRYMMHFCGSLIHPQW 60
DB 69 VITAAHCGPVDVKTALTRVQREOHLYYQDQLPVSRIIYHPQFYIIQTGADIALLELE 128
61 VITAAHCGPVDVKTALTRVQREOHLYYQDQLPVSRIIYHPQFYIIQTGADIALLELE 120
DB 129 EVVNISSRVHTVTLPPASSTFPFGMPGVCWTGMDVNDDEPLPPFPPLKQVPIEMENHC 188
121 EVVNISSRVHTVTLPPASSTFPFGMPGVCWTGMDVNDDEPLPPFPPLKQVPIEMENHC 180
DB 189 DAKYHLGAYTGDVRIIRDDMLCAGNSORDSCCKDGGPVLCKVNGTWLQAGVSWDGGC 248
181 DAKYHLGAYTGDVRIIRDDMLCAGNSORDSCCKDGGPVLCKVNGTWLQAGVSWDGGC 240
DB 249 AQPNRPGIYTRVTVYLDWIHHYVPPKP 275
241 AQPNRPGIYTRVTVYLDWIHHYVPPKP 267

RESULT 9
US-09-917-254-101

/ Sequence 101, Application US/09917254

/ Patent No. 6703204

/ GENERAL INFORMATION:

/ APPLICANT: Mutter, George

/ APPLICANT: Baek, Jan

/ TITLE OF INVENTION: Prognostic Classification of Breast Cancer

/ FILE REFERENCE: B0801/7224(JRV)

/ CURRENT APPLICATION NUMBER: US/09/917,254

/ CURRENT FILING DATE: 2001-07-27

/ PRIOR APPLICATION NUMBER: US 60/222,093

/ PRIOR FILING DATE: 2000-07-28

/ NUMBER OF SEQ ID NOS: 102

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 101

/ LENGTH: 267

/ TYPE: PRT

/ ORGANISM: Homo Sapiens

US-09-917-254-101

Query Match 92.2%; Score 1394; DB 4; Length 267;

Best Local Similarity 93.3%; Pred. No. 3e-140; Mismatches 11; Indels 0; Gaps 0;

Matches 249; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

DB 9 LPTLASRAVAAPAPVQALQAGIVGGQAPRSKMPQVSLRVDRYMMHFCGSLIHPQW 68
1 LPTLASRAVAAPAPVQALQAGIVGGQAPRSKMPQVSLRVDRYMMHFCGSLIHPQW 60
DB 69 VITAAHCGPVDVKTALTRVQREOHLYYQDQLPVSRIIYHPQFYIIQTGADIALLELE 128
61 VITAAHCGPVDVKTALTRVQREOHLYYQDQLPVSRIIYHPQFYIIQTGADIALLELE 120
DB 129 EVVNISSRVHTVTLPPASSTFPFGMPGVCWTGMDVNDDEPLPPFPPLKQVPIEMENHC 188
121 EVVNISSRVHTVTLPPASSTFPFGMPGVCWTGMDVNDDEPLPPFPPLKQVPIEMENHC 180
DB 189 DAKYHLGAYTGDVRIIRDDMLCAGNSORDSCCKDGGPVLCKVNGTWLQAGVSWDGGC 248
181 DAKYHLGAYTGDVRIIRDDMLCAGNSORDSCCKDGGPVLCKVNGTWLQAGVSWDGGC 240
DB 249 AQPNRPGIYTRVTVYLDWIHHYVPPKP 275
241 AQPNRPGIYTRVTVYLDWIHHYVPPKP 267

RESULT 10
US-08-944-483-69

/ Sequence 69, Application US/08944483

/ Patent No. 6232456

/ GENERAL INFORMATION:

/ APPLICANT: COHEN, MAURICE

/ APPLICANT: COLPITTS, TRACEY L.

/ APPLICANT: FRIEDMAN, PAULA N.

/ APPLICANT: GRAMADOS, EDWARD N.

/ APPLICANT: KLAUS, MICHAEL R.

/ APPLICANT: RUSSELL, JOHN C.

/ APPLICANT: STEWART, KENT D.

/ APPLICANT: STROUPE, STEVEN D.

/ TITLE OF INVENTION: NOVEL SEQUENCE PROTEASE REAGENTS

/ TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

/ NUMBER OF SEQUENCES: 76

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Abbott Laboratories

/ STREET: 100 Abbott Park Road

/ CITY: Abbott Park

/ STATE: IL

/ COUNTRY: USA

/ ZIP: 60064-3500

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette

/ COMPUTER: IBM Compatible

```

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
;
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 62324566
;
; US-08-944-483-69
```

```

Query Match          90.8%; Score 1373; DB 3; Length 245;
Best Local Similarity 100.0%; Pred. No. 4,6e-138;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 31 IYGGQAPRSKMPQVSLRVDRYWMHFCGSLIHPQWVLTAAHCLGPDVVDLATLRVQL 90
    |||||
DB 1 IYGGQAPRSKMPQVSLRVDRYWMHFCGSLIHPQWVLTAAHCLGPDVVDLATLRVQL 60
    |||||
QY 91 REQHLYYQDQLPVSRILVHPQFYIIQTGADIALLEBPVNISRVHTVWLPPASETFP 150
    |||||
DB 61 REQHLYYQDQLPVSRILVHPQFYIIQTGADIALLEBPVNISRVHTVWLPPASETFP 120
    |||||
QY 151 PGMPCWVTGWDVNDDEPLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIIRDML 210
    |||||
DB 121 PGMPCWVTGWDVNDDEPLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIIRDML 180
    |||||
QY 211 CAGNSQRDSCGDSGGLVCKVNGTWLQAGVYSWDEGCAQPNRPGLIYRTVYLLDMITHY 270
    |||||
DB 181 CAGNSQRDSCGDSGGLVCKVNGTWLQAGVYSWDEGCAQPNRPGLIYRTVYLLDMITHY 240
    |||||
QY 271 VPKKP 275
    |||||
DB 241 VPKKP 245
```

```

RESULT 11
US-09-079-970A-6
; Sequence 6, Application US/09079970A
; Patent No. 6274366
;
; GENERAL INFORMATION:
; APPLICANT: Mafitt, Mark A.
; APPLICANT: Niles, Andrew L.
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: Enzymatically-Active Recombinant Human
; TITLE OF INVENTION: Beta-Trypsin and Method of Making Same
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property Department
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,970A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506.073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-09-079-970A-6
```

```

Query Match          84.9%; Score 1284; DB 3; Length 245;
Best Local Similarity 92.7%; Pred. No. 1,4e-128;
Matches 227; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
```

```

QY 31 IYGGQAPRSKMPQVSLRVDRYWMHFCGSLIHPQWVLTAAHCLGPDVVDLATLRVQL 90
    |||||
DB 1 IYGGQAPRSKMPQVSLRVDRYWMHFCGSLIHPQWVLTAAHCLGPDVVDLATLRVQL 60
    |||||
QY 91 REQHLYYQDQLPVSRILVHPQFYIIQTGADIALLEBPVNISRVHTVWLPPASETFP 150
    |||||
DB 61 REQHLYYQDQLPVSRILVHPQFYIIQTGADIALLEBPVNISRVHTVWLPPASETFP 120
    |||||
QY 151 PGMPCWVTGWDVNDDEPLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIIRDML 210
    |||||
DB 121 PGMPCWVTGWDVNDDEPLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIIRDML 180
    |||||
QY 211 CAGNSQRDSCGDSGGLVCKVNGTWLQAGVYSWDEGCAQPNRPGLIYRTVYLLDMITHY 270
    |||||
DB 181 CAGNRRDSCGDSGGLVCKVNGTWLQAGVYSWDEGCAQPNRPGLIYRTVYLLDMITHY 240
    |||||
QY 271 VPKKP 275
    |||||
DB 241 VPKKP 245
```

```

RESULT 12
US-09-601-318-1
; Sequence 1, Application US/09601318
; Patent No. 6613769
;
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Gesellschaft z. Fnd. d. Wissensch. e.V
; APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
; APPLICANT: Bode, Wolfram
; APPLICANT: Moroder, Luis
; APPLICANT: Pereira, Pedro Jose Barbosa
; APPLICANT: Bergner, Andreas
; APPLICANT: Huber, Robert
; APPLICANT: Sommerhoff, Christian
; APPLICANT: Schachke, No. 6613769bert
; APPLICANT: Br, Thomas
; APPLICANT: Martin, Thomas
; APPLICANT: Stadlwieser, Josef
; APPLICANT: Ulrich, Wolf-Rdiger
; APPLICANT: Dominik, Andreas
; APPLICANT: Thubaut, Ulrich
; APPLICANT: Bundschuh, Daniela
; APPLICANT: Beume, Rolf
; APPLICANT: Goedel, Karl-Josef
; TITLE OF INVENTION: Trypsin-Inhibitors
; FILE REFERENCE: 17674P WO-1
; CURRENT APPLICATION NUMBER: US/09/601,318
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: DE19804761.4
```


PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: DE19851300.3
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 245
TYPE: PRT
ORGANISM: Homo sapiens
US-09-601-318-1

Query Match 84.9%; Score 1284; DB 4; Length 245;
Best Local Similarity 92.7%; Pred. No. 1.4e-128;
Matches 227; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 31 IVGGGEAPRSKMPQVSLRVDRYMMHFCGSLIHPQWVLTAAHCLGPDVCDLATLAVQL 90
DB 1 IVGGGEAPRSKMPQVSLRVDRYMMHFCGSLIHPQWVLTAAHCLGPDVCDLATLAVQL 60
QY 91 REQHLYYQDOLLPSRIIVHPQFYTAQIGADIALLEBPVKSSSHVHTVTLPPASETFP 150
DB 61 REQHLYYQDOLLPSRIIVHPQFYTAQIGADIALLEBPVKSSSHVHTVTLPPASETFP 120
QY 151 PGMPCWVTGMGDVNDDEPLPPFPPLKQVVPIMENHICDAKYHLGAYTGDDVRIIRDML 210
DB 121 PGMPCWVTGMGDVNDDEPLPPFPPLKQVVPIMENHICDAKYHLGAYTGDDVRIIRDML 180
QY 211 CAGNSQDSCKDSGGPLVCKVNGTWTLOAGVSWDEGCAQPNRPGLIYTRVYIYDMIHRY 270
DB 181 CAGNTRRDS CGDSGGPLVCKVNGTWTLOAGVSWDEGCAQPNRPGLIYTRVYIYDMIHRY 240
QY 271 VPKKP 275
DB 241 VPKKP 245

RESULT 13
US-09-079-970A-5
Sequence 5, Application US/09079970A
Patent No. 6274366
GENERAL INFORMATION:
APPLICANT: Maflet, Mark A.
APPLICANT: Miles, Andrew L.
APPLICANT: Haak-Frendescho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
NUMBER OF SEQUENCES: 6
TITLE OF INVENTION: Beta-Trypsin and Method of Making Same
CORRESPONDENCE ADDRESS:
ADDRESSER: Intellectual Property Department
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34506.073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-079-970A-5

Query Match 84.9%; Score 1284; DB 3; Length 249;
Best Local Similarity 92.7%; Pred. No. 1.5e-128;
Matches 227; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 31 IVGGGEAPRSKMPQVSLRVDRYMMHFCGSLIHPQWVLTAAHCLGPDVCDLATLAVQL 90
DB 5 IVGGGEAPRSKMPQVSLRVDRYMMHFCGSLIHPQWVLTAAHCLGPDVCDLATLAVQL 64
QY 91 REQHLYYQDOLLPSRIIVHPQFYTAQIGADIALLEBPVKSSSHVHTVTLPPASETFP 150
DB 65 REQHLYYQDOLLPSRIIVHPQFYTAQIGADIALLEBPVKSSSHVHTVTLPPASETFP 124
QY 151 PGMPCWVTGMGDVNDDEPLPPFPPLKQVVPIMENHICDAKYHLGAYTGDDVRIIRDML 210
DB 125 PGMPCWVTGMGDVNDDEPLPPFPPLKQVVPIMENHICDAKYHLGAYTGDDVRIIRDML 184
QY 211 CAGNSQDSCKDSGGPLVCKVNGTWTLOAGVSWDEGCAQPNRPGLIYTRVYIYDMIHRY 270
DB 185 CAGNTRRDS CGDSGGPLVCKVNGTWTLOAGVSWDEGCAQPNRPGLIYTRVYIYDMIHRY 244
QY 271 VPKKP 275
DB 245 VPKKP 249

RESULT 14
US-09-601-318-4
Sequence 4, Application US/09601318
Patent No. 6613769
GENERAL INFORMATION:
APPLICANT: Max-Planck-Gesellschaft z. Fnd. d. Wissensch. e.V.
APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
APPLICANT: Bode, Wolfram
APPLICANT: Moroder, Luis
APPLICANT: Pereira, Pedro Jose Barbosa
APPLICANT: Bergner, Andreas
APPLICANT: Huber, Robert
APPLICANT: Sommerhoff, Christian
APPLICANT: Schaschke, No. 6613769bert
APPLICANT: Br, Thomas
APPLICANT: Martin, Thomas
APPLICANT: Stadlwieser, Josef
APPLICANT: Ulrich, Wolf-Rdiger
APPLICANT: Dominik, Andreas
APPLICANT: Thibaut, Ulrich
APPLICANT: Beumel, Rolf
APPLICANT: Beumel, Rolf
APPLICANT: Goebel, Karl-Josef
TITLE OF INVENTION: Trypsin-Inhibitors
FILE REFERENCE: 17674P WO-1
CURRENT APPLICATION NUMBER: US/09/601,318
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: DE19804761.4
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: DE19851300.3
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-601-318-4

Query Match 84.5%; Score 1277; DB 4; Length 244;
Best Local Similarity 92.6%; Pred. No. 7.9e-128;
Matches 226; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

```
QY 31 IVGGQAPRSKMPWQVSLRVDRYMMHFCGSLIHPQWVLTAAHCLGPDVKDIATLRVOL 90
DB 1 IVGGQAPRSKMPWQVSLRVHGRPYMMHFCGSLIHPQWVLTAAHCVGPVKDIAALRVOL 60
QY 91 REQHLVYQDQLPVSRILVHPQFYIIQTGADIALLEBEPVNISSRVHTVMLPPASSTPP 150
DB 61 REQHLVYQDQLPVSRILVHPQFYIIQTGADIALLEBEPVNISSRVHTVMLPPASSTPP 120
QY 151 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIIRDML 210
DB 121 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIIRDML 180
QY 211 CAGNSQDSCSKGDSGGPVLCKVNGTWLQAGVVSMDGCAQPNRPGIYTRVTYLLDMIHNY 270
DB 181 CAGNTRRDSGQDSGGPVLCKVNGTWLQAGVVSMDGCAQPNRPGIYTRVTYLLDMIHNY 240
QY 271 VPKK 274
DB 241 VPKK 244
```

```
RESULT 15
US-09-601-318-5
; Sequence 5, Application US/09601318
; Patent No. 6613769
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Gesellschaft z. Ftd. d. Wissenssch. e.V
; APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
; APPLICANT: Bode, Wolfram
; APPLICANT: Moroder, Luis
; APPLICANT: Pereira, Pedro Jose Barbosa
; APPLICANT: Bergner, Andreas
; APPLICANT: Huber, Robert
; APPLICANT: Sommerhoff, Christian
; APPLICANT: Schaschke, No. 6613769bert
; APPLICANT: Br. Thomas
; APPLICANT: Martin, Thomas
; APPLICANT: Stadlmaier, Josef
; APPLICANT: Ulrich, Wolf-Rüdiger
; APPLICANT: Dominik, Andreas
; APPLICANT: Thibaut, Ulrich
; APPLICANT: Bundschuh, Daniela
; APPLICANT: Beume, Rolf
; APPLICANT: Goebel, Karl-Josef
; TITLE OF INVENTION: Tryptase-Inhibitor
; FILE REFERENCE: 17674P WO-1
; CURRENT APPLICATION NUMBER: US/09/601,318
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: DE19804761.4
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: DE19851300.3
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-318-5
```

```
Query Match 84.5%; Score 1277; DB 4; Length 244;
Best Local Similarity 92.6%; Pred. No. 7, 9e-128;
Matches 226; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 31 IVGGQAPRSKMPWQVSLRVDRYMMHFCGSLIHPQWVLTAAHCLGPDVKDIATLRVOL 90
DB 1 IVGGQAPRSKMPWQVSLRVHGRPYMMHFCGSLIHPQWVLTAAHCVGPVKDIAALRVOL 60
QY 91 REQHLVYQDQLPVSRILVHPQFYIIQTGADIALLEBEPVNISSRVHTVMLPPASSTPP 150
DB 61 REQHLVYQDQLPVSRILVHPQFYIIQTGADIALLEBEPVNISSRVHTVMLPPASSTPP 120
QY 151 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIIRDML 210
```

```
DB 121 PGMPCWVTGMDVNDERLPPFPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIIRDML 180
QY 211 CAGNSQDSCSKGDSGGPVLCKVNGTWLQAGVVSMDGCAQPNRPGIYTRVTYLLDMIHNY 270
DB 181 CAGNTRRDSGQDSGGPVLCKVNGTWLQAGVVSMDGCAQPNRPGIYTRVTYLLDMIHNY 240
QY 271 VPKK 274
DB 241 VPKK 244
```

```
Search completed: August 27, 2005, 23:31:26
Job time : 64 secs
```

CC (see also AAV44328). The invention

This is the deduced amino acid sequence of human mast cell trypsinase alpha (see also AAV4328). The invention provides: compositions comprising an isolated trypsinase-7 that may include chimeric proteins that contain (a) a

CC human trypsinase for all but the active site region and (b) the substrate-
 CC binding pocket of mouse trypsinase-7 or its homologues (see AAW64233-39); a
 CC method for treating a blood clot by administering a nucleic acid molecule
 CC that codes for a trypsinase-7, or an expression product, to decrease
 CC fibrinogen activity; a nucleic acid encoding a serine protease (SP); and
 CC a method of producing a mature SP by expressing the inactive zymogen in a
 CC host cell, and cleaving the enterokinase susceptibility domain. The
 CC trypsinase-7 polypeptides can be used to treat disorders mediated by
 CC undesirable thrombus clot formation such as myocardial infarction and
 CC reocclusion following angioplasty of blood clots associated with
 CC pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, renal
 CC vein and peripheral arterial thrombosis. They are also useful for all
 CC surgical procedures that require decreased blood clots

CC Sequence 275 AA:

Query Match 100.0%; Score 1512; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1.2e-131;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLILLALPVLASRAVAAPVQALQOAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
 Db 1 MSLILLALPVLASRAVAAPVQALQOAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
 QY 61 GSIIHPQWVLTAAHCLGPDVVDLTLRVQLREOHLYYQDQLPVSRITVHPQFYIIQTGA 120
 Db 61 GSIIHPQWVLTAAHCLGPDVVDLTLRVQLREOHLYYQDQLPVSRITVHPQFYIIQTGA 120
 QY 121 DIALLELEBPVNISSRVHTVMLPPASSTFPFGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
 Db 121 DIALLELEBPVNISSRVHTVMLPPASSTFPFGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
 QY 181 PIMENHICDAKYLGAATGDDVRIIRDMLCAGNSQBSCKGDSGGLVCKVNGTWMLOAG 240
 Db 181 PIMENHICDAKYLGAATGDDVRIIRDMLCAGNSQBSCKGDSGGLVCKVNGTWMLOAG 240
 QY 241 VVSMDEGCAQPNRPGLYTRVTYYLDMIHVYPKKP 275
 Db 241 VVSMDEGCAQPNRPGLYTRVTYYLDMIHVYPKKP 275

RESULT 2

AAW63173
 ID AAW63173 standard; protein; 275 AA.

AC AAW63173;

DT 27-OCT-1998 (first entry)

DE Human mast cell trypsinase alpha polypeptide.

KM Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
 KM trypsinase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
 KM antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
 KM hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
 KM inflammatory skin condition; human; mast cell trypsinase alpha.

OS Homo sapiens.

PN WO9833812-A1.

PD 06-AUG-1998.

PF 30-JAN-1998; 98MO-US001865.

PR 05-FEB-1997; 97US-0037090P.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PI Stevens RL, Huang C;

PR WPI; 1998-437390/37.

DR N-PSDB; AAV42710.

XX Trypsinase-6 complex inhibitory peptides - used to treat mast cell-mediated
 PT inflammatory disorders e.g. asthma.
 XX
 XX Disclosure; Page 45-46; 69pp; English.

XX This reexamines the human mast cell trypsinase alpha protein which is a
 CC homologue of the mouse mast cell protease (mMCP-6) zymogen. The invention
 CC provides sequences shown in AAW63160 to AAW63169 that are inhibitors of
 CC mMCP-6. These peptides which are trypsinase-6 complex inhibitors, can be
 CC used for treating a mast cell-mediated inflammatory disorder. The
 CC inhibitors can be used to treat inflammatory disorders including asthma,
 CC allergic rhinitis, urticaria and antioedema, eczematous dermatitis
 CC (atopic dermatitis), anaphylaxis, hyperproliferative skin disease, peptic
 CC ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory
 CC skin conditions

SQ Sequence 275 AA:

Query Match 100.0%; Score 1512; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1.2e-131;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLILLALPVLASRAVAAPVQALQOAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
 Db 1 MSLILLALPVLASRAVAAPVQALQOAGIVGGEAPRSKMPQVSLRVDRYMMHFCG 60
 QY 61 GSIIHPQWVLTAAHCLGPDVVDLTLRVQLREOHLYYQDQLPVSRITVHPQFYIIQTGA 120
 Db 61 GSIIHPQWVLTAAHCLGPDVVDLTLRVQLREOHLYYQDQLPVSRITVHPQFYIIQTGA 120
 QY 121 DIALLELEBPVNISSRVHTVMLPPASSTFPFGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
 Db 121 DIALLELEBPVNISSRVHTVMLPPASSTFPFGMPGCVTGMGDVNDDEPLPPFPFLKQYKV 180
 QY 181 PIMENHICDAKYLGAATGDDVRIIRDMLCAGNSQBSCKGDSGGLVCKVNGTWMLOAG 240
 Db 181 PIMENHICDAKYLGAATGDDVRIIRDMLCAGNSQBSCKGDSGGLVCKVNGTWMLOAG 240
 QY 241 VVSMDEGCAQPNRPGLYTRVTYYLDMIHVYPKKP 275
 Db 241 VVSMDEGCAQPNRPGLYTRVTYYLDMIHVYPKKP 275

RESULT 3

ADK52588
 ID ADK52588 standard; protein; 275 AA.

AC ADK52588;

DT 06-MAY-2004 (first entry)

DE Hematological disorder associated Gene ID 1847 encoded protein.

KM cytostatic; antianemic; antistickling; virucide; hemostatic; nephrotropic;
 KM cytostatic; thrombolytic; antiparasitic; gene therapy;
 KM hematologic disorder; cancer; Sickle Cell Anemia;
 KM Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;
 KM Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;
 KM transfusion reaction; Erythroblastosis; mechanical trauma;
 KM micro-angiopathic hemolytic anemia; parasite infection.

OS Homo sapiens.

PN WO2003065871-A2.

PD 14-AUG-2003.

PF 28-JAN-2003; 2003WO-US002484.

PR 04-FEB-2002; 2002US-0354333P.

PR 28-FEB-2002; 2002US-0360258P.

PR 15-MAR-2002; 2002US-0364476P.

[illegible]

AC	ADP12448;
XX	
DT	12-AUG-2004 (first entry)
DE	Protein encoded by mRNA of the invention #58.
XX	
KW	transplant rejection; immune system; rheumatoid arthritis; lupus;
KW	inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX	
OS	Homo sapiens.
PN	WO2004042346-A2.
XX	
PD	21-MAY-2004.
XX	
PF	24-APR-2003; 2003WO-US012946.
PR	24-APR-2002; 2002US-00131831.
XX	
PR	20-DEC-2002; 2002US-00325899.
XX	
PA	(EXPR-) EXPRESSION DIAGNOSTICS INC.
XX	
PI	Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI	Rosenberg S;
XX	
DR	WPI: 2004-400724/37.
PT	Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT	pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT	rejection, in an individual, comprises detecting the expression level of
PT	the genes.
XX	
PS	Claim 65; SEQ ID NO 2457; 1762bp; English.
CC	The present invention relates to diagnosing or monitoring transplant
CC	rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC	comprises detecting the expression level of one or more genes. The
CC	method, system and kits are useful in diagnosing or monitoring
CC	transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC	islet, lung, bone marrow or stem cell transplant rejection,
CC	xenotransplant rejection or mechanical organ replacement rejection, in an
CC	individual. The method is also useful in assessing the immune status of
CC	an individual. The methods are also useful in diagnosing and monitoring
CC	diseases that involve the immune system, e.g. rheumatoid arthritis,
CC	lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC	viral, bacterial or fungal infection. The present sequence represents a
CC	protein that is encoded by the mRNA of the invention.
XX	
SQ	Sequence 275 AA;
Query Match	100.0%; Score 1512; DB 8; Length 275;
Best Local Similarity	100.0%; Pred. No. 1.2e-131;
Matches 275; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
DG	1 MSLILLALPLVLAASAAVAAPAVQLQAAGIVCGEABRSKMPQVSLRVDRYMHFGC 60
QY	
DG	1 MSLILLALPLVLAASAAVAAPAVQLQAAGIVCGEABRSKMPQVSLRVDRYMHFGC 60
QY	61 GSLIHPQWLTAACHLGPVDKIATLRVQLREOHLYYDQDLLPVSRILVHPOFYIIQTGA 120
DG	61 GSLIHPQWLTAACHLGPVDKIATLRVQLREOHLYYDQDLLPVSRILVHPOFYIIQTGA 120
QY	121 DIALLEBEPVNISSRVHTVMLPASFTFPPQMPCWVTGWGDVNDDELPPFPFLKYKV 180
DG	121 DIALLEBEPVNISSRVHTVMLPASFTFPPQMPCWVTGWGDVNDDELPPFPFLKYKV 180
QY	181 PTMEWHICDAKHGLGAYTGDDVRIRDMCLCAGNSQRSCSGDGSGPLVCVKNGTWLAG 240
DG	181 PTMEWHICDAKHGLGAYTGDDVRIRDMCLCAGNSQRSCSGDGSGPLVCVKNGTWLAG 240
QY	241 VVSMDEGCAPRPRIYTRVTYYLDWIHHYVPKKP 275
DG	241 VVSMDEGCAPRPRIYTRVTYYLDWIHHYVPKKP 275

RESULT 5
ADP56070
ID ADP56070 standard; protein; 275 AA.
XX
XX
AC ADP56070;
XX
XX 18-NOV-2004 (first entry)
XX
DE Human PRO protein sequence SEQ ID NO:2046.
XX
XX human; PRO; immune related disease; inflammatory immune response;
KM immune response stimulation; antiallergic; antianaemic; antiarthritic;
KM antileukemic; antidiabetic; antiinflammatory; antipsoriatic;
KM antitubercular; antihypertensive; CNS; dermatological; gastrointestinal;
KM haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KM nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KM virulicide; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2004039956-A2.
XX
XX 13-MAY-2004.
PD
PF 28-OCT-2003; 2003WO-US034381.
XX
PR 29-OCT-2002; 2002US-0422472P.
XX
XX (GENTH) GENENTECH INC.
XX
PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
XX WPI: 2004-376182/35.
DR N-PSDB; ADP56069.
XX
XX New PRO polynucleotides and polypeptides, useful in useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.
XX
PS Claim 1; SEQ ID NO 2046; 3009pp; English.
XX
XX The present invention describes an isolated PRO nucleic acid (1). Also
CC described: (1) a vector comprising (1); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptide; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC, and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianaemic, antiarthritic,
CC antileukemic, antidiabetic, antiinflammatory, antipsoriatic,
CC antitubercular, antihypertensive, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virulicide activities, and can be used in gene therapy. The nucleic acid
CC (1) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO protein from the present invention.
XX

SEQ Sequence 275 AA;
Query Match 100.0%; Score 1512; DB 8; Length 275;
Best Local Similarity 100.0%; Pred. No. 1,2e-131;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLILLALPVLASRAVAPAVQALQAGIVGGEAPRSKWPQVSLRDRYMMHFCG 60
DB 1 MSLILLALPVLASRAVAPAVQALQAGIVGGEAPRSKWPQVSLRDRYMMHFCG 60
QY 61 GSLIHPOWLTAHCLGPDVQDLATLRVQLRECHLYYDQDLVSRILVHPQYIIQFGA 120
DB 61 GSLIHPOWLTAHCLGPDVQDLATLRVQLRECHLYYDQDLVSRILVHPQYIIQFGA 120
QY 121 DIALLELEBPVNISSRVHTVM.LPASETFPPGMPQVWGVDNDDEPLPPFPPLKQVKV 180
DB 121 DIALLELEBPVNISSRVHTVM.LPASETFPPGMPQVWGVDNDDEPLPPFPPLKQVKV 180
QY 181 PIMENHICDAKTHLGAAYTGDDVRIIRDMLCAGNSQSDSCGSGPLVCXVNGTWLQAG 240
DB 181 PIMENHICDAKTHLGAAYTGDDVRIIRDMLCAGNSQSDSCGSGPLVCXVNGTWLQAG 240
QY 241 VWSDEGCAQPNRPGLYTRVVTYLLDMHHVYPKKP 275
DB 241 VWSDEGCAQPNRPGLYTRVVTYLLDMHHVYPKKP 275
RESULT 6
ADE62892
ID ADE62892 standard; protein; 275 AA.
XX
XX ADE62892;
AC
XX 29-JAN-2004 (first entry)
DT
XX Human Protein P15157, SEQ ID NO 8826.
DE
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KM spared nerve injury; SNL; Chung.
XX
OS Homo sapiens.
XX
XX WO2003016475-A2.
PN
XX 27-FEB-2003.
PD
XX 14-AUG-2002; 2002WO-US025765.
PF
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI: 2003-268312/26.
DR GENBANK; P15157.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
PS Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

S0 Sequence 275 AA;

Query Match 99.5%; Score 1505; DB 7; Length 275;

Best Local Similarity 99.3%; Pred. No. 5.5e-133; Mismatches 0; Gaps 0;

Matches 273; Conservative 2; Indels 0; Gaps 0;

QY 1 MLSTLLALPVLASRAVAAPAPVQALQAGIVGGGEAPRSKMPQVSLRVDRYMHFCG 60

Db 1 MLSTLLALPVLASRAVAAPAPVQALQAGIVGGGEAPRSKMPQVSLRVDRYMHFCG 60

QY 61 GSLLHPQVNLTAHCLGPDVVDLALTRVQLREQLHYTODQLPVSRIIVHQPFIITQGA 120

Db 61 GSLLHPQVNLTAHCLGPDVVDLALTRVQLREQLHYTODQLPVSRIIVHQPFIITQGA 120

QY 121 DIALLEBEPNISRVTVMTPPASETFPPGMPGVCWTGMDVNDDEPLPPFPPLKQYKV 180

Db 121 DIALLEBEPNISRVTVMTPPASETFPPGMPGVCWTGMDVNDDEPLPPFPPLKQYKV 180

QY 121 DIALLEBEPNISRVTVMTPPASETFPPGMPGVCWTGMDVNDDEPLPPFPPLKQYKV 180

Db 121 DIALLEBEPNISRVTVMTPPASETFPPGMPGVCWTGMDVNDDEPLPPFPPLKQYKV 180

QY 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNSQSDSCGDSGGLVCKVNGTWTLOAG 240

Db 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNSQSDSCGDSGGLVCKVNGTWTLOAG 240

QY 241 VVSWDEGCAQPNRPGLITRYVYLLDWIHHYVPKKP 275

Db 241 VVSWDEGCAQPNRPGLITRYVYLLDWIHHYVPKKP 275

RESULT 7

ADE56171

ID ADE56171 standard; protein; 275 AA.

AC ADE56171;

DT 29-JAN-2004 (first entry)

DE Human Protein XP_018104, SEQ ID NO 2020.

XX Human; pain; neuronal tissue; gene therapy;

XX spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002MO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

PA (PARR) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX MPI: 2003-268312/26.

XX GENBANK; XP_018104.

PT New composition comprising two or more isolated polypeptides, useful for

PS preparing a medicament for treating pain in an animal.

PS Claim 1; Page: 1017p; English.

CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

S0 Sequence 275 AA;

Query Match 94.6%; Score 1430; DB 7; Length 275;

Best Local Similarity 93.5%; Pred. No. 4.9e-124; Mismatches 257; Conservative 8; Indels 0; Gaps 0;

QY 1 MLSTLLALPVLASRAVAAPAPVQALQAGIVGGGEAPRSKMPQVSLRVDRYMHFCG 60

Db 1 MLSTLLALPVLASRAVAAPAPVQALQAGIVGGGEAPRSKMPQVSLRVDRYMHFCG 60

QY 61 GSLLHPQVNLTAHCLGPDVVDLALTRVQLREQLHYTODQLPVSRIIVHQPFIITQGA 120

Db 61 GSLLHPQVNLTAHCLGPDVVDLALTRVQLREQLHYTODQLPVSRIIVHQPFIITQGA 120

QY 121 DIALLEBEPNISRVTVMTPPASETFPPGMPGVCWTGMDVNDDEPLPPFPPLKQYKV 180

Db 121 DIALLEBEPNISRVTVMTPPASETFPPGMPGVCWTGMDVNDDEPLPPFPPLKQYKV 180

QY 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNSQSDSCGDSGGLVCKVNGTWTLOAG 240

Db 181 PIMENHICDAKYHLGAYTGDDVRIIRDMLCAGNSQSDSCGDSGGLVCKVNGTWTLOAG 240

QY 241 VVSWDEGCAQPNRPGLITRYVYLLDWIHHYVPKKP 275

Db 241 VVSWDEGCAQPNRPGLITRYVYLLDWIHHYVPKKP 275

RESULT 8

ADJ94864

ID ADJ94864 standard; protein; 275 AA.

DB 241 VWSWEGCAQPNRPGLYTRVYLDIMHHVPPKP 275
|||||
RESULT 9
ADJ19871
ID ADJ19871 standard; protein; 275 AA.
AC ADJ19871;
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2690.
DE
XX
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
KM
XX Homo sapiens.
OS
XX WO2004048938-A2.
PN
XX 10-JUN-2004.
PD
XX 26-NOV-2003; 2003WO-US038193.
PF
XX 26-NOV-2002; 2002US-0429739P.
PR
XX (PROT-) PROTEIN DESIGN LABS INC.
PA
XX Aziz N, Ginsburg WM, Zlotnick A;
PI
XX WPI; 2004-441208/41.
DR
XX
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX Example 2, SEQ ID NO 2690; 210pp; English.
PS
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
CC
XX
XX Sequence 275 AA;
SQ
Query Match 93.3%; Score 1411; DB 8; Length 275;
Best Local Similarity 92.4%; Pred. No. 2,9e-122;
Matches 254; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
OY 1 MSLILLALPVLASRYAAPAPQALQKRVIGGQAPRSKPMQVSLVHGPRYMHFPG 60
DB 1 MNLILLALPVLASRYAAPAPQALQKRVIGGQAPRSKPMQVSLVHGPRYMHFPG 60
OY 61 GSLLHPQWVLTAAHCLGPDVKDLATLRVLRQHLVYQDLVPSRIIVHPQFYIIQTGA 120
DB 61 GSLLHPQWVLTAAHCLGPDVKDLATLRVLRQHLVYQDLVPSRIIVHPQFYIIQTGA 120
OY 121 DIALLEBEPVNISRYHTVMLPPASSTPPGMPGCVTGWGDVNDDEPLPPPPPLKQVAV 180
DB 121 DIALLEBEPVNISRYHTVMLPPASSTPPGMPGCVTGWGDVNDDEPLPPPPPLKQVAV 180
OY 181 PTMENNHCADAKYHLGAYTGDDVRIIRDMLCAGNSRDSCKGSGGLVCKNGTWLQAG 240
DB 181 PTMENNHCADAKYHLGAYTGDDVRIIRDMLCAGNSRDSCKGSGGLVCKNGTWLQAG 240

DB 181 PTMENNHCADAKYHLGAYTGDDVRIIRDMLCAGNSRDSCKGSGGLVCKNGTWLQAG 240
OY 241 VWSWEGCAQPNRPGLYTRVYLDIMHHVPPKP 275
DB 241 VWSWEGCAQPNRPGLYTRVYLDIMHHVPPKP 275
|||||
RESULT 10
ADJ94866
ID ADJ94866 standard; protein; 275 AA.
AC ADJ94866;
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Novel NOVX protein sequence #47.
DE
XX
XX antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KM anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KM neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KM antiarthritic; antiinflammatory; dermatological; antiasthmatic;
KM antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KM infectious disease; cancer; cardiovascular disease;
KM hypertension; atherosclerosis; neurodegenerative disorder;
KM Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KM osteoarthritis; hematopoietic disorder; inflammatory skin disorder;
KM asthma; dyslipidemia; neurogenesis; cell differentiation;
KM cell proliferation; hematopoiesis; wound healing; angiogenesis;
KM chromosome mapping; tissue typing; pharmacogenomic.
XX
XX Homo sapiens.
OS
XX WO2003040325-A2.
PN
XX 15-MAY-2003.
PD
XX
XX 05-NOV-2002; 2002WO-US035464.
PF
XX
XX 05-NOV-2001; 2001US-0338626P.
PR 06-NOV-2001; 2001US-0333072P.
PR 09-NOV-2001; 2001US-0348283P.
PR 15-NOV-2001; 2001US-0335610P.
PR 16-NOV-2001; 2001US-0338543P.
PR 20-NOV-2001; 2001US-0331630P.
PR 20-NOV-2001; 2001US-0331641P.
PR 21-NOV-2001; 2001US-0332152P.
PR 27-NOV-2001; 2001US-0333912P.
PR 28-NOV-2001; 2001US-0334027P.
PR 29-NOV-2001; 2001US-0334300P.
PR 30-NOV-2001; 2001US-0334421P.
PR 30-NOV-2001; 2001US-0334526P.
PR 04-DEC-2001; 2001US-0336576P.
PR 04-DEC-2001; 2001US-0336664P.
PR 07-DEC-2001; 2001US-0338314P.
PR 07-DEC-2001; 2001US-0338390P.
PR 10-DEC-2001; 2001US-0339006P.
PR 10-DEC-2001; 2001US-0339008P.
PR 11-DEC-2001; 2001US-0339286P.
PR 01-FEB-2002; 2002US-0353280P.
PR 01-FEB-2002; 2002US-0353288P.
PR 04-FEB-2002; 2002US-0354392P.
PR 04-FEB-2002; 2002US-0354393P.
PR 04-FEB-2002; 2002US-0354409P.
PR 27-FEB-2002; 2002US-0359944P.
PR 27-FEB-2002; 2002US-0360148P.
PR 05-MAR-2002; 2002US-0361790P.
PR 05-MAR-2002; 2002US-0361833P.
PR 05-MAR-2002; 2002US-0361925P.
PR 05-MAR-2002; 2002US-0362230P.
PR 05-MAR-2002; 2002US-0362625P.
PR 13-MAR-2002; 2002US-0364000P.
PR 13-MAR-2002; 2002US-0364181P.

PR 13-MAR-2002; 2002US-0364182P.
 PR 13-MAR-2002; 2002US-0364197P.
 PR 13-MAR-2002; 2002US-0364227P.
 PR 17-MAY-2002; 2002US-0381621P.
 PR 28-MAY-2002; 2002US-0383675P.
 PR 17-JUL-2002; 2002US-0396703P.
 PR 06-AUG-2002; 2002US-0401552P.
 PR 07-AUG-2002; 2002US-0401594P.
 PR 07-AUG-2002; 2002US-0401787P.
 PR 15-AUG-2002; 2002US-0403619P.
 PR 20-AUG-2002; 2002US-0404821P.
 PR 23-AUG-2002; 2002US-0405368P.
 PR 23-AUG-2002; 2002US-0405402P.
 PR 23-AUG-2002; 2002US-0405466P.
 PR 23-AUG-2002; 2002US-0405631P.
 PR 26-AUG-2002; 2002US-0406125P.
 PR 04-NOV-2002; 2002US-00287226.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Agee M, Alsobrook JF, Berghs C, Boldog FL, Burgess CE, Chant JS;
 PI Chaudhuri A, Dipippo VA, Edinger SR, Eissen A, Ellemann K;
 PI Gangoli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NY;
 PI Li L, Malyanck Uman, Macdougall JR, Mezes PS, Miller CE, Millet I;
 PI Ooi CE, Ott T, Padigaru M, Patuturajan M, Rastelli L, Rieger DK;
 PI Rotherberg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ;
 PI Vernet CAM, Zernsen BD, Zhong M;
 XX
 DR MPI; 2003-441551/41.
 DR N-PSDB; ADJ94865.
 XX
 PT New isolated NOXV polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOXV-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.
 XX
 PS Claim 1; SEQ ID NO 94; 800pp; English.
 XX
 CC The invention relates to novel isolated polypeptides, mature forms of
 CC these, or a sequence that is at least 95 % identical to, or having one or
 CC more conservative amino acid substitutions in the polypeptides. The
 CC polypeptides, nucleic acid molecules and antibodies are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOXV-associated disorder. The nucleic acid
 CC molecules, polypeptides and antibodies are useful for treating,
 CC preventing or diagnosing diseases such as metabolic disorders, diabetes,
 CC obesity, infectious diseases (viral, bacterial, fungal, helminthic, and
 CC protozoal), anorexia, cancer, cardiovascular diseases (hypertension,
 CC atherosclerosis), neurodegenerative disorders, Alzheimer's disease,
 CC Parkinson's disease, epilepsy, immune disorders (osteoarthritis),
 CC hematopoietic disorders, inflammatory skin disorders, asthma, and various
 CC dyslipidemias. The nucleic acids and polypeptides may also be used as
 CC targets for the identification of small molecules that modulate or
 CC inhibit e.g. neurogenesis, cell differentiation, cell proliferation,
 CC hematopoiesis, wound healing and angiogenesis, in gene therapy, in
 CC generation of antibodies that bind immunospecifically to NOXV substances
 CC for use in therapeutic or diagnostic methods. The nucleic acids are
 CC further used as hybridization probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. This sequence
 CC corresponds to one of the NOXV polypeptides of the invention.
 XX
 SO Sequence 275 AA;
 Query Match 92.9%; Score 1405; DB 7; Length 275;
 Best Local Similarity 92.0%; Pred. No. 1e-121;
 Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

DB 61 GSIHPQWVLTAAHCVPVCKDLATLRVQLREOHLYYDQQLPVSRITVHPQFYTAQIGA 120
 QY 121 DIALLELEBPVNISSRVHTVMTLPASSETFPDGMPCVTVGWGDVNDDEPLPPFPKQYKV 180
 DB 121 DIALLELEBPVAVSSHVHTVTLPPASSETFPDGMPCVTVGWGDVNDDEPLPPFPKQYKV 180
 QY 181 PIMENHICDAKYHLCAYTGDDVRIIRDMTLCAGNSQSDSCKDSGGPVCYKNGTWLQAG 240
 DB 181 PIMENHICDAKYHLCAYTGDDVRIIRDMTLCAGNTRRSDSCGDSGGPVCYKNGTWLQAG 240
 QY 241 VVSWDEGCAQPNRPGLYTRVTVYLLPMHHVYVKKP 275
 DB 241 VVSWDEGCAQPNRPGLYTRVTVYLLPMHHVYVKKP 275
 RESULT 11
 ADKS2590
 ID ADKS2590 standard; protein; 275 AA.
 XX
 AC ADKS2590;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Hematological disorder associated Gene ID 1849 encoded protein.
 XX
 KW cytostatic; anti-anemic; antisticking; virucide; hemostatic; nephrotropic;
 KW hemostatic; thrombolytic; antiparasitic; gene therapy;
 KW hematologic disorder; cancer; Sickle Cell Anemia;
 KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;
 KW Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;
 KW transfusion reaction; Erythroblastosis; mechanical trauma;
 KW micro-angiopathic hemolytic anemia; parasite infection.
 XX
 OS Homo sapiens.
 XX
 PN WO2003065871-A2.
 XX
 PD 14-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-US002484.
 XX
 PR 04-FEB-2002; 2002US-0354333P.
 PR 28-FEB-2002; 2002US-0360258P.
 PR 15-MAR-2002; 2002US-0364476P.
 PR 26-APR-2002; 2002US-0375626P.
 PR 06-JUN-2002; 2002US-0386494P.
 PR 24-JUN-2002; 2002US-0390965P.
 PR 28-JUN-2002; 2002US-0392480P.
 PR 03-JUL-2002; 2002US-0394128P.
 PR 31-JUL-2002; 2002US-0399783P.
 PR 13-AUG-2002; 2002US-0403221P.
 PR 30-AUG-2002; 2002US-0407045P.
 PR 25-NOV-2002; 2002US-0429048P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Carroll JM, Healy A, Welch NS, Kelly LM;
 PI
 DR MPI; 2003-731464/69.
 DR N-PSDB; ADKS2589.
 XX
 PT Identifying a compound capable of treating a hematologic disorder (e.g.
 PT anemia or leukemia) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 131,148, 199 or 12303
 PT polypeptide or nucleic acid.
 XX
 PS Disclosure; SEQ ID NO 48; 232pp; English.
 XX
 CC The invention relates to a method of identifying a compound capable of
 CC treating a hematologic disorder comprises assaying the ability of the
 CC compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677,
 CC 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
 CC 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic

CC acid expression or polypeptide activity, thus, identifying a compound
 CC capable of treating a hematologic disorder. The methods are useful in
 CC diagnosing, preventing and treating hematological disorders, such as
 CC cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia,
 CC Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders
 CC associated with an increased risk of Thrombosis, Herpes, Thalassemia,
 CC antibody-mediated disorders such as transfusion reactions and
 CC Erythroblastosis, mechanical trauma to red blood cells such as micro-
 CC angopathic hemolytic anemias, infections by parasites or chemical
 CC injuries. The methods may also be used for identifying compounds that
 CC modulate hematological disorders. This sequence corresponds to the
 CC protein encoded by one of the genes modulated by the compounds.

XX Sequence 275 AA;

Query Match 92.9%; Score 1405; DB 7; Length 275;

Best Local Similarity 92.0%; Pred. No. 1e-121;
 Matches 253; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSLTLLALPVLASRAVAAPVQALQAGIVGQGEAPRSKMPQVSLRYRDRYMMHFCG 60
 DB 1 MNLTLALPVLASRAVAAPVQALQAGIVGQGEAPRSKMPQVSLRYRDRYMMHFCG 60
 QY 61 GSLHPQWVLTAAHCLGPDVXDALTFRVQLREQHLYYODQLPVSRITVHPQYIIQTGA 120
 DB 61 GSLHPQWVLTAAHCLGPDVXDALTFRVQLREQHLYYODQLPVSRITVHPQYIIQTGA 120
 QY 121 DIALLEBEPVNISRVTMTLPPASETFPPGMPGVTGMDVNDDEPLPPFPPLKQYKV 180
 DB 121 DIALLEBEPVNISRVTMTLPPASETFPPGMPGVTGMDVNDDEPLPPFPPLKQYKV 180
 QY 181 PTMENNICDAKHYLGAVTGDDVRIIRDMLCAGNSQDSCKGDSGGLVCKVGTMLQAGV 240
 DB 181 PTMENNICDAKHYLGAVTGDDVRIIRDMLCAGNSQDSCKGDSGGLVCKVGTMLQAGV 240
 QY 241 VVSWEGCAQPNRPGLYTRVTYYLDMIHIVPKKP 275
 DB 241 VVSWEGCAQPNRPGLYTRVTYYLDMIHIVPKKP 275

RESULT 12

AAW64238 standard; protein; 273 AA.

AC AAW64238;
 XX 24-NOV-1998 (first entry)
 DT Human mast cell tryptase I.
 XX
 DE Human mast cell tryptase I.
 XX
 KW Mast cell tryptase I; human; MCP-7; mast cell protease 7; blood clot;
 KW anticoagulant; myocardial infarction; reocclusion; thromboembolism;
 KW cerebral embolism; thrombosis; therapy.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..18
 FT Peptide /label= Sig_peptide
 FT Peptide 19..28
 FT Peptide /label= Pro_peptide
 FT Protein 29..273
 FT Protein /label= Mat_protein

XX MO9824886-A1.

XX 11-JUN-1998.

XX 25-NOV-1997; 97WO-US021620.

XX 04-DEC-1996; 96US-0032354P.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX Stevens RL;

XX WPI; 1998-333306/29.

XX N-PSDB; AAW44329.

XX New compositions containing tryptase-7, e.g. mouse mast cell protease-7 -
 XX are used to treat clot formation in e.g. myocardial infarction,
 XX reocclusion following angioplasty or pulmonary thrombo-embolism.
 XX Disclosure; Page 65; 92pp; English.

XX This is the deduced amino acid sequence of human mast cell tryptase I
 XX (see also AAW44329). The invention provides: compositions comprising an
 XX isolated tryptase-7 that may include chimeric proteins that contain (a) a
 XX human tryptase for all but the active site region and (b) the substrate-
 XX binding pocket of mouse tryptase-7 or its homologues (see AAW64233-39); a
 XX method for treating a blood clot by administering a nucleic acid molecule
 XX that codes for a tryptase-7, or an expression product, to decrease
 XX fibrinogen activity; a nucleic acid encoding a serine protease (SP); and
 XX a method of producing a mature SP by expressing the inactive zymogen in a
 XX host cell, and cleaving the enterokinase susceptibility domain. The
 XX tryptase-7 polypeptides can be used to treat disorders mediated by
 XX undesirable thrombus clot formation such as myocardial infarction and
 XX reocclusion following angioplasty of blood clots associated with
 XX pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, renal
 XX vein and peripheral arterial thrombosis. They are also useful for all
 XX surgical procedures that require decreased blood clots

XX Sequence 273 AA;

Query Match 92.7%; Score 1402; DB 2; Length 273;

Best Local Similarity 92.3%; Pred. No. 1.9e-121;
 Matches 252; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 3 SLLTLALPVLASRAVAAPVQALQAGIVGQGEAPRSKMPQVSLRYRDRYMMHFCGS 62
 DB 1 MNLTLALPVLASRAVAAPVQALQAGIVGQGEAPRSKMPQVSLRYRDRYMMHFCGS 60
 QY 63 LIHPQWVLTAAHCLGPDVXDALTFRVQLREQHLYYODQLPVSRITVHPQYIIQTGADI 122
 DB 61 LIHPQWVLTAAHCLGPDVXDALTFRVQLREQHLYYODQLPVSRITVHPQYIIQTGADI 120
 QY 123 ALLELEBEPVNISRVTMTLPPASETFPPGMPGVTGMDVNDDEPLPPFPPLKQYVPI 182
 DB 121 ALLELEBEPVNISRVTMTLPPASETFPPGMPGVTGMDVNDDEPLPPFPPLKQYVPI 180
 QY 183 MENNICDAKHYLGAVTGDDVRIIRDMLCAGNSQDSCKGDSGGLVCKVGTMLQAGV 242
 DB 181 MENNICDAKHYLGAVTGDDVRIIRDMLCAGNSQDSCKGDSGGLVCKVGTMLQAGV 240
 QY 243 SWEGCAQPNRPGLYTRVTYYLDMIHIVPKKP 275
 DB 241 SWEGCAQPNRPGLYTRVTYYLDMIHIVPKKP 273

RESULT 13

AAW63174 standard; protein; 273 AA.

AC AAW63174;
 XX 27-OCT-1998 (first entry)
 DT Human mast cell tryptase I polypeptide.
 XX
 DE Human mast cell tryptase I polypeptide.
 XX
 KW Mast cell protease; MCP; mouse; inhibitor; peptidic substrate; asthma;
 KW tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
 KW antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
 KW hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
 KW inflammatory skin condition; human; mast cell tryptase I.
 XX
 OS Homo sapiens.

This Page Blank (uspto)